



Db 121 SSSSLGCKVLRKH 134

RESULT 2

ID R04087 standard; protein: 134 AA.

AC R04087;

DT 01-JUN-1990 (first entry)

DE Protein encoded by human natriuretic related peptide.

KW Porcine BNP; natriuretic; diuretic; vasodilator; hypertension.

OS Sus scrofa.

FT Key Location/Qualifiers

FT region 44..45

FT /label=Join between first and second exon

FT 130

FT /label=Join between second and third exon

PN WO8912069-A.

14-DEC-1989.

31-MAY-1989; 02373.

31-MAY-1988; US-200383.

14-JUN-1988; US-2006470.

PR 19-JAN-1989; US-299880.

PA (CALB) Calif Biotech Inc.

PI Seilhamer JJ, Lewicki J, Scarborough RM, Porter GJ;

DR N-PDB; 002852.

PT New natriuretic and vasodilator peptides - obtd. using cDNA sequence

PS encoding porcine brain natriuretic peptide and related human canine genes

PS Example 5; Fig. 5; 61bp; English.

CC Sequences derived from porcine brain natriuretic gene can be used in part

CC as probes to isolate similar genes from different species. Although human

CC natriuretic related peptides (NRP) could not be isolated directly, canine

CC NRPs could be, and these could then be used as probes to their human

CC equivalents. Here the gene product is shown, taken from the plasmid

CC phBMP-1.

CC Sequence 134 AA:

Sequence 134 AA:

Query Match 100.0%; Score 690; DB 1; Length 134;

Best Local Similarity 100.0%; Pred. No. 8.1e-63;

Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 mdpqtapsra11111flhafiqrshp1gspgsadletsq1gqgrnhlgk1selqve 60

|||||

DB 1 MDPQTAPSRALL1LFLHLAF1GGRSHPLGSPGSASDLETSGLQGRNHLQK1SELOVE 60

61 qtsleplgesprrtgvkxrevateg1rghrkmylytlrapspkmyvgsgc1gfkmdr1 120

|||||

DB 61 QTSLEPLGESPRRTGVKXREVATEG1RGHRKMYLYTLRAPSPKMYVGS1GCGFRKMDRI 120

QY 121 ssssg1gckv1rrh 134

|||||

DB 121 SSSSLGCKVLRKH 134

RESULT 3

ID Y05325

AC Y05325;

DT 25-JUN-1999 (first entry)

DE Human gamma-BNP protein sequence.

KW Gamma-BNP; human; brain natriuretic protein; immunoassay; heart disease;

OS Homo sapiens.

PN WO913331-A1.

18-MAR-1999.

PF 10-SEP-1998; J04063.

PR 11-SEP-1997; JP-246684.

PA (SHIO) SHIONOGI & CO LTD.

PI Asada H, Endou K, Shimizu H;

DR WPI; 99-243746/20.

DR N-PDB; X33826.

PT Sandwich immuno assay for mammalian gamma BNP

PS Claim 2; Page 20-21; 24pp; Japanese.

CC This sequence is the human gamma-BNP (brain natriuretic protein).

CC The invention relates to an immunoassay method specific for mammalian

CC gamma-BNP derivatives, which comprises the use of a first antibody

CC reacting with mammalian alpha-BNP and a second antibody with preprio or

CC gamma-BNP derivatives but not with alpha-BNP. The immunoassay is useful

CC for diagnosing and monitoring heart diseases, particularly cardiac

CC insufficiency. The technique uses only blood plasma, and is simple,

CC stable and reliable.

CC Sequence 134 AA:

Query Match 100.0%; Score 690; DB 1; Length 134;

Best Local Similarity 100.0%; Pred. No. 8.1e-63;

Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 mdpqtapsra11111flhafiqrshp1gspgsadletsq1gqgrnhlgk1selqve 60

|||||

DB 1 MDPQTAPSRALL1LFLHLAF1GGRSHPLGSPGSASDLETSGLQGRNHLQK1SELOVE 60

61 qtsleplgesprrtgvkxrevateg1rghrkmylytlrapspkmyvgsgc1gfkmdr1 120

|||||

DB 61 QTSLEPLGESPRRTGVKXREVATEG1RGHRKMYLYTLRAPSPKMYVGS1GCGFRKMDRI 120

QY 121 ssssg1gckv1rrh 134

|||||

DB 121 SSSSLGCKVLRKH 134

RESULT 4

ID R04084

AC R04084;

DT 01-JUN-1990 (first entry)

DE Oligopeptide encoded by porcine brain natriuretic peptide cDNA.

KW Porcine BNP; natriuretic; diuretic; vasodilator; hypertension.

OS Sus scrofa.

FT Key Location/Qualifiers

FT region 41..42

FT /label=Join of first and second exons.

FT 127

FT /label=Join of second and third exons.

FT 106..131

FT mat.peptide

PN WO8912069-A.

PD 14-DEC-1989.

PF 31-MAY-1989; 02373.

PR 31-MAY-1988; US-200383.

PR 14-JUN-1988; US-2006470.

PR 19-JAN-1989; US-299880.

PA (CALB) Calif Biotech Inc.

PI Seilhamer JJ, Lewicki J, Scarborough RM, Porter GJ;

DR WPI; 90-007453/01.

DR N-PDB; 002845.

PT New natriuretic and vasodilator peptides - obtd. using cDNA sequence

PT encoding porcine brain natriuretic peptide and related human canine genes

PS Example 1; Fig. 1; 61bp; English.

CC Sequences derived from porcine brain natriuretic gene can be used in part

CC as probes to isolate similar genes from different species. Although human

CC natriuretic related peptides (NRP) could not be isolated directly, canine

CC NRPs could be, and these could then be used as probes to their human

CC equivalents.

CC Sequence 131 AA:

Query Match 48.5%; Score 334.5; DB 1; Length 131;

Best Local Similarity 53.0%; Pred. No. 7.4e-27;

Matches 71; Conservative 20; Mismatches 40; Indels 3; Gaps 2;

QY 1 mdpqtapsra11111flhafiqrshp1gspgsadletsq1gqgrnhlgk1selqve 60

|||||

DB 1 MDPQTAPSRALL1LFLHLAF1GGRSHPLGSPGSASDLETSGLQGRNHLQK1SELOVE 60

61 qtsleplgesprrtgvkxrevateg1rghrkmylytlrapspkmyvgsgc1gfkmdr1 120

|||||

DB 61 QTSLEPLGESPRRTGVKXREVATEG1RGHRKMYLYTLRAPSPKMYVGS1GCGFRKMDRI 120

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Db      58 RRDLEPLNQDRRLQENAEAREAPGVGLPRSSIFQVYLNGIRSPKMTMRSGCGRHLDR I 117
Oy      121 ssssglgckvyltrh 134
          | ||||| |||||
Db      118 GSLSGLGCVLRRY 131

RESULT      5
R07342
ID    R07342 standard; protein: 131 AA.
AC    R07342;
DT    29-JAN-1991 (first entry)
DE    Porcine Brain Natriuretic Peptide.
KM    Porcine Brain Natriuretic peptide (BNP).
OS    Sus scrofa domestica.
FH    key Location/Qualifiers
FT    misc_difference 26..26
       /label=H or Y

J02222683-A.
05-SEP-1990
22-FEB-1989; 042720.
22-FEB-1989; JP-042720.
PA (DAUC ) DAIIICHI PHARM CO LTD.
PA (DAII-) DAIIICHI KAGAKU YAKUHIN.
WP1: 90-315501/42.
DR     NP-BSDb; Q06197.
DN     DNA contg. swine brain natriuretic peptide - is produced in large
PT     amts.
PS     Disclosure; Fig 5; 8pp; Japanese.
CC     cDNA encoding porcine BNP was isolated from mRNA obtained from swine
CC     atrial fibrillation. The nucleotide at position 170 is a pyrimidine.
CC     The ambiguity leads to two possible protein sequences, one
CC     containing His at the corresponding site and the other containing
CC     Tyr. The CDS is claimed.
SQ     Sequence 131 AA;

```

Query Match	47.2%	Score 325.5;	DB 1;	Length 131;
Best Local Similarity	52.2%	Pred. No. 66-26;		
Matches 70;	Conservative 20;	Mismatches 41;	Indels 3;	Gaps 2

  

QY	1	m d p q t a p e r a l l i l l f i n h a f i g r s h p l g p s g s a d l e t s g l q e g r n h l g k l s e l y w e	60
DB	1	MGPPRALPR-VLLTLFLHLLLCGRSXPGGAGLASEL--PGIQELIDRLRDRVSSELOA	57
QY	61	q t s l a p l g e s p p t g v w k s r e v a t e g i g r h k m v l y t l r a p i s p k m v g s g c f g r i m d r l	120
DB	58	RTDEPLNODKRLTAWMERKAPPGVGLGPRSSIFVYLNGIRNSPKIRMSGCGCRRLDRI	117
QY	121	s s s s g l g c k v l i r t h	134
DB	118	GSLSGLCNVLRXY	131

  

RESULT	6
R04086	
AC	R04086 standard; protein; 131 AA.
ID	R04086;
DE	01-JUN-1990 (first entry)
DT	Protein encoded by canine natriuretic related peptide.
KM	Porcine BNP; natriuretic; diuretic; vasodilator; hypertension.
OS	Sus scrofa.
FT	Key
FT	region
FT	region
FT	region
PN	W08912069-A.
PD	14-DEC-1989.
PF	31-MAY-1989;
PR	31-MAY-1988;
PR	14-JUN-1988;

  

Location/Qualifiers	
42..43	
/label=join between first and second exon	
127	
/label=join between second and third exon	

PR 19-JAN-1989; US-2939880.  
PA (CALB) Calif Biotech Inc.  
PI Sellhammer JJ, Lewicki J, Scarborough RM, Porter GU;  
DR WPI; 90-007453/01.  
N-PSDB; 002852.  
PT New natriuretic and vasodilator peptides - obtd. using cDNA sequence  
encoding porcine brain natriuretic peptide and related human canine genes  
Example 4; Fig.3; 61pp; English.  
PS Although human natriuretic related peptides (NRP) could not be isolated  
CC directly, canine NRPs could be, and these could then be used as probes to  
CC their human equivalents.  
CC See also 002845.  
SQ Sequence 131 AA;

Query Match	42.0%	Score 289.5	DB 1	Length 131
Best Local Similarity	50.7%	Pred. No. 2.7e-22		
Matches	69	Conservative	13	Mismatches 47
				Indels 7
				Gaps 3

RESULT	7
TD	R62682
AC	R62682 standard; protein; 122 AA.
DT	14-JUL-1995 (first entry)
DE	Hamster brain natriuretic peptide (BNP).
KW	Brain natriuretic peptide; detection; vaccines.
OS	Cricetulus griseus.
FH	Key Location/Qualifiers
FT	disulfide_bond 100..116
FT	peptide 1..26
FT	/label= sig_peptide
PN	J06279496-A.
PD	04-OCT-1994.
PF	25-MAR-1993; 067113.
PR	25-MAR-1993; JP-067113.
PA	(SHIO.) SHIONOGI & CO LTD.
WP	WPI; 94-354771/44.
DR	N-PSDB; Q73026.
PT	Hamster brain derived natriuretic peptide(s) - useful for the
PT	detection of BNPs, and in vaccine production
PS	Claim 1; Page 5; 8pp; Japanese.
CC	Q73026 encodes R62682 hamster brain natriuretic peptide (BNP).
CC	R62682 can be used for the detection and determination of BNP,
CC	which is useful for various reagents and medicines.
QO	Sequence 122 AA;

	Query Match	28.3%	Score 195;	DB 1:	Length 122;
	Best Local Similarity	35.5%;	Pred. No. 8.9e-13;		
	Matches 50; Conservative	23;	Mismatches 42;	Indels 26;	Gaps 4;
QY	1 mddptapralllllflnlaifgrshpbgpsasdietsglqgrnhlgklselgve	60			
Dd	1 MDLRVLSRVVLFLFLFVLSPLGSHPLGSSQPE-----GSKM-----	42			
QY	61 qtslejpdesrptc--vsksevat---egltghkmvlyltrprspkhmgsgcf	113			
Dd	42 QTLDLIRKAEAAVAAGQLKDQDVTIAPLQGSTLGSDSTLHVQLKLRNSKKHNSGCF	101			
QY	114 grkmdrtssssglcgckvlirrh	134			

DB 102 GQRDRIGSFRLGCVLKR 122

## RESULT 8

R72812  
ID R72812 standard; protein; 175 AA.  
AC R72812;  
DE 19-DEC-1995 (first entry)  
DE Gamma-IFN/glucagon/BNP fusion protein.  
KW Gamma-IFN/glucagon/BNP; fusion protein; peptide isolation method;  
KW granule forming protein; protease cleavage; E. coli;  
KW B-type natriuretic peptide; gamma-interferon;  
KW recombinant production.  
OS Homo sapiens.  
PN J07090000-A.  
PD 04-APR-1995.  
DE 22-SEP-1993; 236732.  
DE 22-SEP-1993; JP-236732.  
DE (SHIO ) SHIONOGI & CO LTD.  
DE WPI: 95-167255/22.  
PT A new method for the isolation of peptide(s) - comprises fusing the  
PT peptide to a granule forming protein and cleaving the peptide from  
PT the resulting fusion protein using a protease.  
PS Example 2: Page 12; 17pp: Japanese.  
CC R72812 is a gamma-IFN/glucagon/BNP fusion protein. It was used  
CC to demonstrate a new method for the isolation of peptides. The  
CC fusion protein is recombinantly produced in transformed E. coli,  
CC the glucagon/BNP is then cleaved from the granule forming protein  
CC gamma-IFN, using a protease. The glucagon can now be isolated  
CC from the cell culture.  
SQ Sequence 175 AA;

Query Match 26.9%; Score 185.5; DB 1; Length 175;  
Best Local Similarity 48.8%; Pred. No. 1.3e-11;  
Matches 42; Conservative 11; Mismatches 18; Indels 15; Gaps 2;

QY 54 lseqlvestslp-----gesprtygwkrereatlgthkmylytlrapskmyg 108

DB 100 VTDLVQKKAHHELIQVMAELSP-----AAKTKRRRSKSLVDFRSESSEPKWQ 149

QY 109 gsgcfgrkmdrlssssglgckvlrth 134

DB 150 GSGCFGRKMDRISSSSGIGCKVLRH 175

## MULT 9

R10973  
ID R10973 standard; protein; 121 AA.  
AC R10973;  
DE 13-MAY-1991 (first entry)  
DE Rat Brain Natriuretic peptide.  
KW BNP; vasodilator; hypertension; congestive heart failure;  
KW renal failure.  
OS Rattus.  
FH Key  
FT peptide 1--26 Location/Qualifiers  
FT /label- signal peptide  
FT /label- mature BNP  
FT protein 27..121  
PN J03022986-A.  
PD 31-JAN-1991.  
PF 19-JUN-1989; 157066.  
PR 19-JUN-1989; JP-157066.  
PA (MATS/) MATSUO H.  
DE WPI: 91-076871/11.  
DR N-PSDB: 010572.  
PT Isolating DNA encoding rat brain natriuretic peptide(s) - for  
PT treating oedema hypertension congestive heart and renal failure  
PS Claim 1; Page 1; 7pp: Japanese.  
CC The N-terminal Met residue is optional. Expression vectors  
CC containing DNA encoding this amino acid sequence are used to

CC transform host cells. The transformants are cultured to produce  
CC brain natriuretic peptide for treating hypertension, etc.  
SQ Sequence 121 AA;

Query Match 24.6%; Score 169.5; DB 1; Length 121;  
Best Local Similarity 36.3%; Pred. No. 3.4e-10;  
Matches 49; Conservative 17; Mismatches 50; Indels 19; Gaps 4;

QY 1 mdpttasralllllflhflggrshpssgsadletsqdegrnhlqklsel--- 58

DB 1 MDLQKVLPPQMLLLFLNLSPLGSHSPLOSPOSPQST-----MQKLELIRE 50

QY 58 qveqtslepiqesprptgwksrevategrthkmylytlrapskmygsgcfgrkm 117

DB 51 KSEMAQRHLSKOGPR-----KELKRVLRSDSAPRIQERL-RNSKMAHSSSCFGOKI 104

QY 118 drlssssglgckvlr 132

DB 105 DRIGAVSRLGCDGLR 119

## RESULT 10

ID R34301 standard; protein; 32 AA.

AC R34301;  
DE 28-JUL-1993 (first entry)

DE Mutated hBNP.  
KW Wild type; Brain natriuretic peptide; BNP; modify; Asp-Pro.  
OS Homo sapiens.  
PN J05056794-A.  
PD 09-MAR-1993.  
DE 03-SEP-1991; 222783.  
DE 03-SEP-1991; JP-222783.  
DE (DAIT-) DAICHI KAGAKU YAKUHIN KK.  
DE (DAUC-) DAICHI PHARM CO LTD.

PT Physiologically active peptide prep. e.g. human brain

PT natriuretic peptide - by culturing transformed cells having gene

PT that encodes fused protein of active and protective peptide(s),

PT collecting and cleaving protein

PS Disclosure; Page 6; 10pp: Japanese.

CC The sequences given in R34301-02 are mutated brain natriuretic

CC peptides (BNP). These peptides have been modified such that the

CC Asp in the N-terminal Asp-Pro linkage may be replaced by Ser or may

CC be deleted.  
SQ Sequence 32 AA;

Query Match 24.5%; Score 169; DB 1; Length 32;  
Best Local Similarity 100.0%; Pred. No. 7.3e-11;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 spkmvgsgcfgrkmdrlssssglgckvlrth 134

DB 1 SPKMVGSGCFGRKMDRISSSSGIGCKVLRH 32

## RESULT 11

ID R36381 standard; protein; 32 AA.

AC R36381;  
DE 29-JUL-1993 (first entry)

DE Recombinant hBNP.  
KW Plasmid; fusion peptide; murine; rat; interleukin 1; IL-1; human;  
KW brain natriuretic peptide; hBNP; recombinant; BNP.

OS Synthetic.

FH Key  
FT misc\_difference 1 Location/Qualifiers

FT /note- "May be absent"

PN J05066581-A.  
PD 23-MAR-1993.  
PF 10-SEP-1991; 230597.

PR 10-SEP-1991: JP-230597.  
PA (DAIT-) DATICHT KAGAKU YAKUOHIN KK.  
PA (DAUC) DATICHT PHARM CO LTD.  
DR WPI: 93-130645/16.  
PT Prepn. of physiologically active peptide without aspartic acid-proline sequence - comprises gene recombination with cell transformation by specified expression vector  
PS Claim 3: Page 6; 17pp; Japanese.  
CC This sequence represents a recombinant human brain natriuretic peptide (hBNP). This protein was encoded by the fragments of plasmids given in Q4110-04 which encode fusion peptides of murine or rat interleukin 1 (IL-1) fused to hBNP. Fusion genes of this kind can be used to CC express recombinant BNP which lacks the Asp-Pro N-terminal bond. The CC Asp residue may be replaced by Ser or may be absent.  
SQ Sequence 32 AA;

Query Match 24.5%; Score 169; DB 1; Length 32;  
Best Local Similarity 100.0%; Pred. No. 7.3e-11;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
103 spkmvgsqcfgrkmdrissssglgckvlrrh 134  
1 SPKMVGSGCFGRKMDRISSSSGLGCKVLRH 32

RESULT 12  
ID R40861 standard; Protein; 32 AA.  
AC R40861;  
DT 14-MAR-1994 (first entry)  
DE BNP, brain natriuretic peptide; transformation; expression;  
KW BNP; cloning; puc119; protease V8.  
OS Homo sapiens.  
PN J05207891-A.  
PD 20-AUG-1993.  
PF 08-MAR-1991: 043641.  
PR 08-MAR-1991: JP-043641.  
PA (SHIO) SHIONOGI & CO LTD.  
DR WPI: 93-297469/38.  
DR N-PSDB; 047829.  
PT Brain natriuretic peptide prepn. - by forming fused peptide PT congl. desired sequence, cleaving with restriction enzyme and PT collecting desired peptide  
PS Discloure; Page 8; 11pp; Japanese.  
CC The prepn. of BNP comprises: (a) obtaining a fused protein CC protein of formula X-Glu-BNP, where X is a leader sequence of 70-110 amino acids (R45761); (b) cleaving the fused protein with a restriction enzyme that can cleave between Glu and BNP.  
CC (c) collecting BNP.  
CC The BNP sequence is shown in (Q47829) and the Glu-BNP sequence CC is given in (Q47831).  
SQ Sequence 32 AA;

Query Match 24.5%; Score 169; DB 1; Length 32;  
Best Local Similarity 100.0%; Pred. No. 7.3e-11;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
103 spkmvgsqcfgrkmdrissssglgckvlrrh 134  
1 SPKMVGSGCFGRKMDRISSSSGLGCKVLRH 32

RESULT 13  
ID W70090 standard; peptide; 32 AA.  
AC W70090;  
DT 28-OCT-1998 (first entry)  
DE Brain natriuretic peptide (BNP) 1.  
KW BNP; brain natriuretic peptide; cardiac hypertrophy; chronic heart failure; ischaemic cardiac disease; arrhythmia;

KW CGMP: pulmonary blood circulation; haemodynamic property.  
OS Unidentified.  
PN W09634636-A1.  
PD 13-AUG-1998.  
PF 05-FEB-1998: J00483.  
PR 05-FEB-1997: JP-022594.  
PA (SUNR) SUNTORY LTD.  
PI Furiya M, Hidaka T, Inomata N, Yamaki A;  
DR WPI: 98-446949/38.  
PT Drug composition comprises natriuretic peptide(s) - for safe PT treatment of cardiac hypertrophy associated diseases and chronic heart failure  
PS Examples: Page 23; 35pp; Japanese.  
CC This represents a brain natriuretic peptide (BNP) sequence. The CC invention provides a composition for treating cardiac diseases associated CC with cardiac hypertrophy. The composition comprises an active ingredient CC capable of binding to the peptide receptor of GC-A and promoting CC production of cGMP. The drug composition may be used clinically to treat CC cardiac diseases caused by cardiac hypertrophy, including chronic heart CC failure, ischaemic cardiac diseases and arrhythmia. The active substance CC can bind to the natriuretic peptide receptor of GC-A and promote CC production of cGMP, effectively preventing cardiac hypertrophy and CC leading to improvement of the pulmonary blood circulation. The substance CC does not affect haemodynamic properties, blood pressure, heart beat and CC urine volume.  
SQ Sequence 32 AA;

Query Match 24.5%; Score 169; DB 1; Length 32;  
Best Local Similarity 100.0%; Pred. No. 7.3e-11;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
103 spkmvgsqcfgrkmdrissssglgckvlrrh 134  
1 SPKMVGSGCFGRKMDRISSSSGLGCKVLRH 32

RESULT 14  
ID W67040 standard; peptide; 32 AA.  
AC W67040;  
DT 15-DEC-1998 (first entry)  
DE Brain natriuretic peptide (BNP).  
KW atrial natriuretic peptide; brain natriuretic peptide; ANP; BNP; renal disorder.  
OS Mammalia.  
FH Key  
FT Region 2..32 "this fragment having a 11pophyllic group attached  
FT Region 3..32 "this fragment having a 11pophyllic group attached  
FT Region 4..32 "this fragment having a 11pophyllic group attached  
FT Region 5..32 "this fragment having a 11pophyllic group attached  
FT Region 6..32 "this fragment having a 11pophyllic group attached  
FT Region 7..32 "this fragment having a 11pophyllic group attached  
FT Region 8..32 "this fragment having a 11pophyllic group attached  
FT Region 9..32 "this fragment having a 11pophyllic group attached  
FT Region 10..32 "this fragment having a 11pophyllic group attached  
FT Disulfide\_bond 10..32 "this fragment having a 11pophyllic group attached  
FT to it is claimed in Claim 33"

Search completed: April 27, 2000, 18:29:23  
Job time: 2793 sec

FT K09845329-A1. /label= disulphide\_bond  
PN 15-OCT-1998.  
PD 06-APR-1998; DR0142.  
PR 04-APR-1997; US-043400.  
PA (NOVO ) NOVO-NORDISK AS.  
PI Hunsfeldt PO, Knudsen LB, Madsen K;  
DR WPI; 98-557474/47  
PT Lipophilic derivatives of atrial and brain natriuretic peptides -  
PT notably as amides, prolong activity, use in hypertension, congestive  
PT heart failure, renal disorders, oedema, and hepatic cirrhosis.  
PS Claim 32: Pages 1-2; 23pp; English.  
CC The invention relates to natriuretic derivatives, containing a lipophilic  
CC substituent attached to any one amino acid residue. Also new are  
CC natriuretic derivatives as above, but with two attached lipophilic  
CC substituents. Atrial natriuretic (ANP) and brain natriuretic (BNP)  
CC peptides are already used in treatment of various diseases, and it is  
CC believed that the lipophilic derivatives will have similar uses. These  
CC diseases include hypertension, congestive heart failure, oedema, renal  
CC disorders, and hepatic cirrhosis. The lipophilic group protects the  
CC peptide from metabolic breakdown. Increasing the duration of action. The  
CC present sequence represents BNP.  
SQ Sequence 32 AA;

Query Match 24.5%; Score 169; DB 1; Length 32;  
Best Local Similarity 100.0%; Pred. No. 7.3e-11;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 103 spkmvgsqcgfgrkmdrissgglgckvllrh 134  
Db 1 SPKMVGSGCGFGRKMDRISSSGGLGCKVLRH 32

RESULT 15  
R35490  
ID R35490 standard; peptide; 33 AA.  
AC R35490;  
DT 26-AUG-1993 (first entry)  
DE Tyr-hBNP.  
KW Human; brain natriuretic peptide; specificity; monoclonal; antibody;  
KW MAb; hBNP; Hydridoma; BC203; label; detection; hBNP/MAB complex.  
OS Synthetic.  
PN EP-542255-A.  
PD 19-MAY-1993.  
PC 12-NOV-1992; 119353.  
PE 14-NOV-1991; JP-326961.  
PI (SHIO ) SHIONOGI SEIRYAKU KK.  
PI Igano K, Inouye K, Kono M, Tsuji T, Yamauchi A;  
DR WPI; 93-160757/20.  
PT Monoclonal antibody recognising the C-terminus of hBNP - for  
PT determining hBNP levels in blood plasma by immunoassay; useful  
PT for diagnosing hypertension  
PS Disclosure; Page 9; 13pp; English.  
CC This sequence represents Tyr-hBNP (human brain natriuretic peptide).  
CC This peptide was used in determining the specificity of a monoclonal  
CC antibody (MAb) which recognises the C-terminal of hBNP. The MAb is  
CC produced by hydridoma BC203 (PERM BP-3515). The Tyr residue had to  
CC be added to the N-terminal of the hBNP as no other Tyr appears  
CC within the molecule and this residue was used to carry a label to  
CC allow detection of the hBNP/MAB complex.  
SQ Sequence 33 AA;

Query Match 24.5%; Score 169; DB 1; Length 33;  
Best Local Similarity 100.0%; Pred. No. 7.6e-11;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 103 spkmvgsqcgfgrkmdrissgglgckvllrh 134  
Db 2 SPKMVGSGCGFGRKMDRISSSGGLGCKVLRH 33



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OM protein - protein search, using sw model

Run on: April 27, 2000, 18:26:25 ; Search time 14.62 Seconds

(without alignments)  
432.332 Million cell updates/sec

Title: PEPI

Perfect score: 690  
Sequence: 1 mdpgtaperalllllllhla.....rkmdrissgslgckvlrrh 134

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 142080 seqs, 47169319 residues

Total number of hits satisfying chosen parameters: 142080

Minimum DB seq length: 0  
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database :  
1: PIR\_62:\*  
2: PIR1:\*  
3: PIR2:\*  
4: PIR3:\*  
5: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	690	100.0	134	1 AMHUB	natriuretic peptid
2	334.5	48.5	131	2 A33873	brain natriuretic
3	328.5	47.6	131	2 A31676	brain natriuretic
4	246.5	35.7	103	2 A41403	aldosterone secret
5	204.5	29.6	105	2 B36736	brain natriuretic
6	171.5	24.9	121	1 A30162	brain natriuretic
7	165.5	24.0	121	2 I49548	brain natriuretic
8	164.5	23.8	121	2 A49144	type-B natriuretic
9	137	19.9	140	1 A31320	alpha-atrial natrl
10	118	17.1	149	1 AMBQ	atrial natriuretic
11	113	17.1	152	1 AMBO	atrial natriuretic
12	113	16.4	151	1 AMHU	natriuretic peptid
13	113	16.4	153	2 S14873	atrial natriuretic
14	109.5	15.9	150	1 S13107	atrial natriuretic
15	106	15.4	27	2 JC1081	brain natriuretic
16	105.5	15.3	153	1 AMRB	atrial natriuretic
17	104	15.1	145	1 JC0947	atrial natriuretic
18	100	14.5	152	1 AMMS	atrial natriuretic
19	97	14.1	152	1 AMRR	atrial natriuretic
20	90.5	13.1	115	1 S15822	natriuretic peptid
21	88	12.8	126	1 A35155	natriuretic peptid
22	87.5	12.7	126	2 S12988	brain natriuretic
23	87	12.6	37	2 S71382	lebetin 2 isoform
24	86.5	12.5	126	1 AMHUC	natriuretic peptid
25	86.5	12.5	126	1 A61244	natriuretic peptid
26	85.5	12.4	126	2 A55688	natriuretic peptid
27	84	12.2	129	1 A54119	C-type natriuretic
28	82.5	12.0	128	2 S14872	atrial natriuretic
29	82	11.9	161	4 I55480	hypothetical natrl

## ALIGNMENTS

## RESULT 1

AMHUB  
natriuretic peptide B precursor - human  
N:Alternate names: brain natriuretic factor-32 (BNF-32); brain natriuretic protein pr  
N:Contains: brain alpha natriuretic peptide; brain gamma natriuretic factor  
C:Species: Homo sapiens (man)  
C:date: 07-Sep-1990 #sequence, revision 02-Dec-1994 #text\_change 18-Jun-1999  
C:Accession: A36736; A30163; A34143; A34661; B34661  
R:Seilhamer, J. J.; Arsten, A.; Miller, J. A.; Lundquist, P.; Scarborough, R. M.; Lawic  
Biochem. Biophys. Res. Commun. 165, 650-658, 1989  
A:Title: Human and canine gene homologs of porcine brain natriuretic peptide.  
A:Reference number: A36736; MUID:90086474  
A:Accession: A36736  
A:Molecule type: DNA  
A:Residues: 1-134 <SEI>  
A:Cross-references: GB:M31776; NID:9179514; PID:AAA35603.1; PID:9179515  
R:Sudoh, T.; Maekawa, K.; Kojima, M.; Minamino, N.; Kangawa, K.; Matsuo, H.  
Biochem. Biophys. Res. Commun. 159, 1427-1434, 1989  
A:Title: Cloning and sequence analysis of cDNA encoding a precursor for human brain n  
A:Reference number: A30163; MUID:89193743  
A:Accession: A30163  
A:Molecule type: mRNA  
A:Residues: 1-134 <SD>  
A:Cross-references: GB:M31776; NID:9179514; PID:AAA35603.1; PID:9179515  
R:Ramakrishna, Y.; Nakao, K.; Mukoyama, M.; Saito, Y.; Ogawa, Y.; Shiono, S.; Inouye,  
FEBS Lett. 259, 341-345, 1990  
A:Title: Isolation and sequence determination of human brain natriuretic peptide in h  
A:Reference number: A34143; MUID:90092577  
A:Accession: A34143  
A:Molecule type: protein  
A:Residues: 103-134 <KAM>  
R:Hino, J.; Tateyama, H.; Minamino, N.; Kangawa, K.; Matsuo, H.  
Biochem. Biophys. Res. Commun. 167, 693-700, 1990  
A:Title: Isolation and identification of human brain natriuretic peptides in cardiac  
A:Reference number: A30161; MUID:90211249  
A:Accession: A34661  
A:Molecule type: protein  
A:Residues: 27-58 <HIN>  
A:Accession: B34661  
A:Molecule type: protein  
A:Residues: 103-134 <H12>  
C:Genetics:  
A:Gene: GDB:NPPR  
A:Cross-references: GDB:127884; OMIM:600295  
A:Map position: 1p36-1p36  
A:Introns: 44/3; 130/1  
C:Superfamily: natriuretic peptide A precursor  
C:Keywords: brain; diuretic; hormone; natriuretic; osmoregulation  
F:1-26/Domain: signal sequence #status predicted <SIG>  
F:27-134/Product: brain gamma natriuretic factor #status experimental <GNF>  
F:103-134/Product: brain alpha natriuretic peptide #status experimental <ANF>  
F:112-128/Disulfide bonds: #status predicted

31	81.5	11.8	118	2	B54119	C-type natriuretic
32	81.5	11.8	1677	2	T14267	Xin protein, stage
33	81	11.7	30	2	S01657	atrial natriuretic
34	80.5	11.7	1319	1	C43735	brain natriuretic
35	78	11.3	22	2	A35418	brain natriuretic
36	77	11.2	36	2	S15821	ventricular natru
37	74.5	10.8	1065	2	T13230	dachshund isoform
38	74.5	10.8	1072	2	T13228	dachshund protein
39	74.5	10.8	1072	2	T13232	dachshund protein
40	74.5	10.8	1074	2	T13229	dachshund protein
41	74.5	10.8	1081	2	T13231	dachshund protein
42	74	10.7	22	2	A36399	C-type natriuretic
43	74	10.7	27	2	A33431	atrial natriuretic
44	74	10.7	786	1	A47547	serine proteinase
45	72	10.4	22	2	JT0581	natriuretic peptid

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Query Match          100.0%; Score 690; DB 1; Length 134;
Best Local Similarity 100.0%; Pred. No. 2,1e-59;
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 mdptapsralllllflhlaflgrshpbgpsasdsletsglqeqrnhlqgklselqve 60
    |||||
Db 1 MDPTAPSRALLLLFLHLAFLLGGRSHPLGSPGSASDLETSGLGQRNHLQGLSELQVE 60

Oy 61 qtsleplqesprpvgwksrevategltgrhkmvlytlraprpskmygsgcfgrkmdr 120
    |||||
Db 61 QTSLEPLQESPRPTGVWKSREVATEGIRGHRKMVLYTLRAPRSPKMYGSGCGFRKMDRI 120

Oy 121 ssssglgckvllrrh 134
    |||||
Db 121 SSSSGLGCKVLLRRH 134

RESULT 2
A33873
brain natriuretic peptide precursor - pig
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 27-Feb-1990 #sequence_revision 27-Feb-1990 #text_change 16-Jul-1999
C:Accession: A33873; A31675
R:Porter, J.G.; Arfsten, A.; Palisi, T.; Scarborough, R.M.; Lewicki, J.A.; Sellhammer, J.
J. Biol. Chem. 264, 6689-6692, 1989
A:Title: Cloning of a cDNA encoding porcine brain natriuretic peptide.
A:Reference number: A33873; MUID:89214071
A:Accession: A33873
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-131 <POR>
A:Cross-references: GB:M2547; GB:J04708; GB:M22477; GB:M22478; NID:g164392; PIDN:AAA310
R:Minamino, N.; Kangawa, K.; Matsuo, H.
Biochem. Biophys. Res. Commun. 157, 402-409, 1988
A:Title: Isolation and identification of a high molecular weight brain natriuretic peptide.
A:Reference number: A31675; MUID:89061743
A:Accession: A31675
A:Status: preliminary
A:Molecule type: Protein
A:Residues: 26-131 <MIN>
C:Superfamily: natriuretic peptide A precursor

Query Match          48.5%; Score 334.5; DB 2; Length 131;
Best Local Similarity 53.0%; Pred. No. 2,6e-25;
Matches 71; Conservative 20; Mismatches 40; Indels 3; Gaps 2;

Oy 1 mdptapsralllllflhlaflgrshpbgpsasdsletsglqeqrnhlqgklselqve 60
    |||||
Db 1 MGPFWALPR-VLLLFLLHLGCRSHPLGAGLASEL--PGIQELDLRLDRVSELQAE 57

Oy 61 qtsleplqesprpvgwksrevategltgrhkmvlytlraprpskmygsgcfgrkmdr 120
    |||||
Db 58 RTDLEPLQODRGLEAWAREAPATGVLPGRSSIFQVLRGIRSPKMYGSGCGFRKMDRI 117

Oy 121 ssssglgckvllrrh 134
    |||||
Db 121 GSLSGLGCKVLLRRY 131

RESULT 3
A31676
brain natriuretic factor precursor - pig
N:Alternate names: brain natriuretic factor 32
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 16-Jul-1999
C:Accession: A31676; A31517; S06359
R:Meekawa, K.; Sudoh, T.; Furusawa, M.; Minamino, N.; Kangawa, K.; Ohkubo, H.; Nakanishi,
Biochem. Biophys. Res. Commun. 157, 410-416, 1988
A:Title: Cloning and sequence analysis of cDNA encoding a precursor for porcine brain na
A:Reference number: A31676; MUID:89061744
A:Accession: A31676

```

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A:Molecule type: mRNA
A:Residues: 1-131 <MAE>
A:Cross-references: GB:M23596; NID:9535704; PIDN:AA859258.1; PID:9535705
R:Sudoh, T.; Minamino, N.; Kangawa, K.; Matsuo, H.
Biochem. Biophys. Res. Commun. 155, 726-732, 1988
A:Title: Brain natriuretic peptide-32: N-terminal six amino acid extended form of bra
A:Reference number: A31517; MUID:88339957
A:Accession: A31517
A:Molecule type: protein
A:Residues: 100-131 <SUD>
R:Sudoh, T.; Kangawa, K.; Minamino, N.; Matsuo, H.
Nature 332, 78-81, 1988
A:Title: A new natriuretic peptide in porcine brain.
A:Reference number: S06359; MUID:88156915
A:Accession: S06359
A:Molecule type: protein
A:Residues: 106-131 <SUD>
C:Superfamily: natriuretic peptide A precursor
C:Keywords: brain; natriuretic
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-131/Product: brain gamma natriuretic factor #status predicted <GAM>
F:100-131/Product: brain alpha natriuretic peptide #status experimental <ALF>
F:109-125/Disulfide bonds: #status experimental

```

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Query Match          47.6%; Score 328.5; DB 2; Length 131;
Best Local Similarity 52.2%; Pred. No. 9,9e-25;
Matches 70; Conservative 21; Mismatches 40; Indels 3; Gaps 2;

Oy 1 mdptapsralllllflhlaflgrshpbgpsasdsletsglqeqrnhlqgklselqve 60
    |||||
Db 1 MGPFWALPR-VLLLFLLHLGCRSHPLGAGLASEL--PGIQELDLRLDRVSELQAE 57

Oy 61 qtsleplqesprpvgwksrevategltgrhkmvlytlraprpskmygsgcfgrkmdr 120
    |||||
Db 58 RTDLEPLQODRGLEAWAREAPATGVLPGRSSIFQVLRGIRSPKMYGSGCGFRKMDRI 117

Oy 121 ssssglgckvllrrh 134
    |||||
Db 121 GSLSGLGCKVLLRRY 131

RESULT 4
A41403
aldosterone secretion inhibitory factor precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 03-Mar-1995
C:Accession: A41403; A30976
R:Nguyen, T.T.; Lazure, C.; Babinski, K.; Chretien, M.; De Lean, A.; Ong, H.
Mol. Endocrinol. 3, 1823-1829, 1989
A:Title: Purification and primary structure of pro-aldosterone secretion inhibitory f
A:Reference number: A41403; MUID:90114187
A:Accession: A41403
A:Molecule type: protein
A:Residues: 1-103 <NGU>
R:Nguyen, T.T.; Lazure, C.; Babinski, K.; Chretien, M.; Ong, H.; de Lean, A.
Endocrinology 124, 1591-1593, 1989
A:Title: Aldosterone secretion inhibitory factor: a novel neuropeptide in bovine chro
A:Reference number: A30976; MUID:89136947
A:Accession: A30976
A:Molecule type: protein
A:Residues: 69-103 <NG2>
C:Superfamily: natriuretic peptide A precursor

Query Match          35.7%; Score 246.5; DB 2; Length 103;
Best Local Similarity 49.1%; Pred. No. 5,6e-17;
Matches 53; Conservative 14; Mismatches 36; Indels 5; Gaps 2;

Oy 27 hplpspsasdsletsglqeqrnhlqgklselqveqtsleplqesprpvgwksrevateg 86
    |||||
Db 1 HPVGGEPVSEL--PGIQELDLRLDRVSELQAEQLNVEFLQDGGGLGEFTWDSFMAAPAG 58

```

**RESULT**

**5**

B36736  
brain natriuretic peptide - dog

C:Species: Canis lupus familiaris (dog)  
C>Date: 19-Apr-1991 #sequence\_revision 19-Apr-1991 #text\_change 09-Dec-1994  
C:Accession: B36736  
R:Seilhamer, J.J.; Artstien, A.; Miller, J.A.; Lundquist, P.; Scarborough, R.M.; Lewicki,  
Biochem. Biophys. Res. Commun. 165, 650-658, 1989  
A>Title: Human and canine gene homologs of porcine brain natriuretic peptide.  
A:Reference number: A36736; MUID:90088474  
A:Accession: B36736  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-105 <SEI>  
A:Cross-references: GB:M31777  
C:Superfamily: natriuretic peptide A precursor

**Query Match**                      29.6%; Score 204.5; DB 2; Length 105;  
**Best Local Similarity**    45.5%; Pred. No. 6.1e-13;  
**Matches**    50; Conservative    11; Mismatches    42; Indels        7; Gaps        3;

Oy     27 hplgpgasadtetsglqeqrnihqgklselqveqtslapiesprptvksrev--at 84  
         |||    |    |    |    |    |    |    |    |    |    |    |    |  
Db     1 HPLGGRSPASG--ASEASELLGLRLKDAVSELQAEGLALEPILHRSHSPA---EAPAGGTP 55  
         |||    |    |    |    |    |    |    |    |    |    |    |    |  
Oy     85 egirghrkmylytlraprskmvgsgcgyrkmdtissssglgcgvrlrh 134  
         |||    |    |    |    |    |    |    |    |    |    |    |    |  
Db     56 RGVLAPHDSVLAALRLRS PKMKHRS GC FGRRLDRIIGSLSGLCNVLRKY 105  
         |||    |    |    |    |    |    |    |    |    |    |    |    |  
**RESULT**        6  
A30162  
brain natriuretic factor precursor - rat

N:Alternate names: brain natriuretic peptide; cardiac natriuretic factor; iso-atrial natu  
N:Contains: brain natriuretic factor BNP-45  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 10-Sep-1989 #sequence\_revision 10-Sep-1989 #text\_change 10-Sep-1989  
C:Accession: A30162; A33691; A54893; A32918; A32919; A33253; A60735; I57704; A33252  
R:Koijima, M.; Minamino, N.; Kangawa, K.; Matsuo, H.  
Biochem. Biophys. Res. Commun. 159, 1420-1426, 1989  
A>Title: Cloning and sequence analysis of cDNA encoding a precursor for rat brain natriu  
A:Reference number: A30162; MUID:89193742  
A:Accession: A30162  
A:Molecule type: mRNA  
A:Residues: 1-121 <KOJ>  
A:Cross-references: GB:M5297; NID:g602483; PIDN:AAA57269.1; PID:g602484  
R:Roy, R.N.; Flynn, T.G.  
Biochem. Biophys. Res. Commun. 171, 416-423, 1990  
A>Title: Organization of the gene for Iso-rANP, a rat B-type natriuretic peptide.  
A:Reference number: A35691; MUID:90365739  
A:Accession: A35691  
A:Molecule type: DNA  
A:Residues: 1-14,'V',16-121 <ROY>  
A:Cross-references: GB:M60731; NID:g204985; PIDN:AAAA1456.1; PID:g204986  
A>Note: The authors translated the codon GTT for residue 15 as Leu  
R:Thierauf, D.J.; Hanford, D.S.; Glombotski, C.C.  
J. Biol. Chem. 269, 17772-17775, 1994  
A>Title: Regulation of rat brain natriuretic peptide transcription. A potential role for  
A:Reference number: A54893; MUID:94299479  
A:Accession: A54893  
A:Molecule type: DNA  
A:Residues: 1-19 <THD>  
A:Cross-references: GB:U02972; NID:g458021; PIDN:AA21648.1; PID:g458022  
R:Ashuraya, M.; Hiro, Y.; Minamino, N.; Kangawa, K.; Matsuo, H.  
Biochem. Biophys. Res. Commun. 163, 226-232, 1989  
A>Title: Isolation and identification of rat brain natriuretic peptides in cardiac atriu  
A:Reference number: A32918; MUID:89374230

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A:Accession: A32918
A:Molecule type: protein
A:Residues: 27-121 <ABU>
R:Kambayashi, Y.; Nakao, K.; Itoh, H.; Hosoda, K.; Saito, Y.; Yamada, T.; Mukoyama, M.; Imura, H.
Biochem. Biophys. Res. Commun. 163, 233-240, 1989
A>Title: Isolation and sequence determination of rat cardiac natriuretic peptide.
A:Reference number: A32919; MUID:89374231
A:Accession: A32919
A:Molecule type: protein
A:Residues: 77-121 <AM>
R:Flynn, T.G.; Brer, A.; Tremblay, L.; Sarda, I.; Lyons, C.; Jennings, D.B.
Biochem. Biophys. Res. Commun. 161, 830-837, 1989
A>Title: Isolation and characterization of iso-rANP, a new natriuretic peptide from r
A:Reference number: A33253; MUID:89286593
A:Accession: A33253
A:Molecule type: protein
A:Residues: 77-119, 'O', 121 <Flx>
R:Nakao, K.; Itoh, H.; Kambayashi, Y.; Hosoda, K.; Saito, Y.; Yamada, T.; Mukoyama, M.
Hypertension 15, 774-778, 1990
A>Title: Rat brain natriuretic peptide. Isolation from rat heart and tissue distribut
A:Reference number: A60735; MUID:90277148
A:Accession: A60735
A:Molecule type: protein
A:Residues: 77-121 <NAK>
R:Daghino, L.; Dirolin, U.; Nemer, M.
Mol. Endocrinol. 5, 1292-1300, 1991
A>Title: Differential expression of natriuretic peptide genes in cardiac and extracardiac tissues.
A:Reference number: 157704; MUID:92123224
A:Accession: 157704
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-121 <RES>
A:Cross-references: GB:M60266; MID:g204983; PIDN:AAA41455.1; PID:g204984
C:Genetics:
A:Introns: 42/3; 117/1
C:Superfamily: natriuretic peptide A precursor
C:Keywords: cardiac muscle; heart
F:1-6/Domain: signal sequence #status predicted <SIG>
F:27-121/Product: brain natriuretic factor #status experimental <MAT1>
F:77-121/Product: brain natriuretic factor BNP-45 #status experimental <MAT2>

Query Match      24.9%; Score 171.5; DB 1; Length 121;
Best Local Similarity 37.1%; Pred. No. 1.le-09;
Matches 49; Conservative 18; Mismatches 52; Indels 13; Gaps 4;

QY      1 mdgptaprrallllflhlafigrshpdpagsasdsletsglqegnhlgkiselqve 60
          ||| | : : : ||||| : : || ||||| : : || : : : || : : : || :
DB       1 MDLQVLPDMLTLFLFLNLSPLGSHPLGSPSOSP--EOSTMKQLLELRKESEMAQR 58
QY      61 qtsleplqesdrptgvwksrevateglgrhkmylytlraprspkmvgsqcgfrkmari 120
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB       59 Q-----LSKDGGPR-----KELKRVLRSQDSARIGERL-RNSKMAHSSSCFGQXDIRI 107
QY      121 ssssglgckvlr 132
          : ||| ||
DB       108 GAVSRLLCGDGLR 119

RESULT      7
149548
brain natriuretic peptide - mouse.
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
C:Accession: I49548
R:Ogawa, Y.; Itoh, H.; Tamura, N.; Suga, S.; Yoshimasa, T.; Uehira, M.; Matsuda, S.;
J. Clin. Invest. 93, 1911-1921, 1994
A>Title: Molecular cloning of the complementary DNA and gene that encode mouse brain
A:Reference number: I49548; MUID:94237953
A:Accession: I49548
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA

```



## RESULT 11

AMBO

atrial natriuretic peptide precursor - bovine  
N:Alternate names: ANP; atrial natriuretic polypeptide

C:Species: Bos primigenius taurus (cattle)

C:Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 18-Jun-1999

C:Accession: A01024; A93049; A24247; A26090

R:Vlasuk, G.P.; Miller, J.; Bensen, G.H.; Lewicki, J.A.

Biochem. Biophys. Res. Commun. 136, 396-403, 1986

A:Title: Structure and analysis of the bovine atrial natriuretic peptide precursor gene.

A:Reference number: A90124; MUID:86215205

A:Accession: A90124

A:Molecule type: DNA

A:Residues: 1-152 &lt;VNA&gt;

A:Cross-references: GB:M3145; NID:g162665; PIDN:AAA30375.1; PID:g162666

R:Omig, H.; McNICOLL, N.; Lazure, C.; Seidah, N.; Chretien, M.; Cantlin, M.; De Lean, A.

Life Sci. 38, 1309-1315, 1986

A:Title: Purification and sequence determination of bovine atrial natriuretic factor.

A:Reference number: A93049; MUID:86173941

A:Accession: A93049

A:Molecule type: Protein

A:Residues: 123-150 &lt;ONG&gt;

C:Genetics:

A:Introns: 40/3; 149/3

C:Superfamily: natriuretic peptide A precursor

C:Keywords: atrium; diuretic; hormone; natriuretic; osmoregulation

F:1-24/Domain: signal sequence #status predicted &lt;SIG&gt;

F:25-153/Product: gamma atrial natriuretic factor #status predicted &lt;ANP&gt;

F:123-150/Product: alpha atrial natriuretic peptide #status experimental &lt;ANP&gt;

F:129-145/Disulfide Bonds: #status predicted

Query Match

Best Local Similarity 17.1%; Score 118; DB 1; Length 152;

Matches 47; Conservative 20; Mismatches 46; Indels 46; Gaps 8;

Db 8 stralllllflhlafl-19grshp19pspsasdlsglqgrhlgk1-----seiq 58

Db 3 SSAIVTSVLFLLAFQPLPOTGAPYGSNSMDLDFKMLRLEDEKMLEDEANVPSQVL 62

Db 59 vevts-----leplqesp-----rptgv-----ksrevateglrhkrhnylt- 98

Db 63 SEQNEAGAPLPLSEMPWMEVNPAPQREGVGLRGPMESD-----RSALTKSK 113

Db 98 ----lrprspkmvqsgscfgfkmrlrissssglgckvlr 132

Db 114 LRAULTAPRS---LRRSSCFGGMRDRIGASGLGCSNFR 149

## RESULT 12

AMHU

natriuretic peptide A precursor - human

N:Alternate names: ANP; atrial natriuretic factor; atrial natriuretic protein; prepronat

C:Contains: atrial alpha natriuretic peptide (ANP); cardiolipatin (atrial gamma natriure

C:Species: Homo sapiens (man)

C:Date: 15-Nov-1994 #sequence\_revision 15-Nov-1994 #text\_change 18-Jun-1999

C:Accession: A22693; B22693; A01424; B29370; A32733; I58054; J14097; I39455; I39459; I39

R:Nemer, M.; Chamberland, M.; Strots, D.; Argentin, S.; Drouin, J.; Dixon, R.A.F.; Zivlin

Nature 312, 654-656, 1984

A:Title: Gene structure of human cardiac hormone precursor, pronatriodilatin.

A:Reference number: A22693; MUID:85061626

A:Accession: A22693

A:Molecule type: DNA

A:Residues: 1-151 &lt;NEM&gt;

A:Cross-references: GB:X01470; NID:g28687; PIDN:CAA25659.1; PID:g823625

A:Accession: B22693

A:Molecule type: DNA

A:Residues: 1-151,'RR' &lt;NE2&gt;

A&gt;Note: allelic variant with UGA termination codon replaced by CGA arginine codon

R:Okawa, S.; Imai, M.; Denc, A.; Tanaka, S.; Noguchi, T.; Nakazato, H.; Kangawa, K.; Fu

Nature 309, 724-726, 1984

A:Title: Cloning and sequence analysis of cDNA encoding a precursor for human atrial nat

A:Reference number: A01424; MUID:84219799

A:Accession: A01424

A:Molecule type: mRNA

A:Residues: 1-151 &lt;OR&gt;

A:Cross-references: GB:K02043; NID:g178629; PIDN:AB59379.1; PID:g178630

R:Seidman, C.E.; Bloch, K.D.; Kiehl, R.A.; Smith, J.A.; Seidman, J.G.

Science 226, 1206-1209, 1984

A:Title: Nucleotide sequences of the human and mouse atrial natriuretic factor genes.

A:Reference number: A29370; MUID:85065766

A:Accession: B29370

A:Molecule type: DNA

A:Residues: 1-64,'D',66-151 &lt;SEI&gt;

A:Cross-references: GB:K02043

A:Reference number: A27733; MUID:84128019

A:Accession: A27733

A:Molecule type: Protein

A:Residues: 124-151 &lt;KAN&gt;

R:Nakayama, K.; Ohkubo, H.; Hirose, T.; Inayama, S.; Nakanishi, S.

Nature 310, 699-701, 1984

A:Title: mRNA sequence for human cardiolipatin-atrial natriuretic factor precursor an

A:Reference number: I58054; MUID:84295577

A:Accession: I58054

A:Molecule type: mRNA

A:Residues: 1-151 &lt;RES&gt;

A:Cross-references: GB:M30262; NID:g180181; PIDN:AAA35669.1; PID:g180182

R:Vaneeste, Y.; Michel, A.; Deschodt-Lanckman, M.

Eur. J. Biochem. 196, 281-286, 1991

A:Title: Hydrolysis of intact and Cys-Phe-cleaved human atrial natriuretic peptide in

A:Reference number: S14097; MUID:91176998

A:Accession: S14097

A:Molecule type: Protein

A:Residues: 124-151 &lt;VAN&gt;

A&gt;Note: natural and synthetic peptide subjected to kallikrein proteolysis

R:Wyllie, R.A.; Condra, J.H.; Dixon, R.A.; Seidah, N.G.; Chretien, M.; Nemer, M.; Cham

Proc. Natl. Acad. Sci. U.S.A. 81, 6325-6329, 1984

A:Title: Molecular cloning and characterization of DNA sequences encoding rat and hum

A:Reference number: I39458; MUID:85038509

A:Accession: I39458

A:Molecule type: mRNA

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Residues: 119-151,'RR' &lt;RE2&gt;

A:Cross-references: GB:K02044; NID:g178631; PIDN:AAA51730.1; PID:g178632

R:Maki, M.; Parmentier, M.; Inagami, T.

Biochem. Biophys. Res. Commun. 125, 797-802, 1984

A:Title: Cloning of genomic DNA for human atrial natriuretic factor.

A:Reference number: I39459; MUID:85069693

A:Accession: I39459

A:Molecule type: DNA

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Residues: 1-75 &lt;REA&gt;

A:Cross-references: GB:K02399; NID:g178633; PIDN:AAA35528.1; PID:g178634

R:Seidman, C.E.; Bloch, K.D.; Zisfein, J.; Smit, J.; Haber, E.; Homay, C.J.; Duby, A.

Hypertension 7, 31-34, 1985

A:Title: Molecular studies of the atrial natriuretic factor gene.

A:Reference number: I39460

A:Accession: I39460

A:Molecule type: DNA

A:Status: translated from GB/EMBL/DBJ

A:Residues: 1-64,'D',66-151 &lt;REA&gt;

A:Cross-references: GB:M54951; NID:g178636; PIDN:AAA35529.1; PID:g178638

R:Greenberg, B.D.; Bensen, G.H.; Seilhammer, J.J.; Lewicki, J.A.; Fliddes, J.C.

Nature 312, 656-658, 1984

A:Title: Nucleotide sequence of the gene encoding human atrial natriuretic factor pre

A:Reference number: I37167; MUID:85061627

A:Accession: I37167

A:Molecule type: DNA

A:Status: translated from GB/EMBL/DBJ

A:Residues: 26-151 &lt;RE5&gt;

A:Cross-references: EMBL:X01471; NID:g28690

C:Comment: Cardiolipatin is a vasoconstrictor but not a diuretic or natriuretic.





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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: April 27, 2000, 18:29:24 ; Search time 8.53 Seconds

(without alignments)  
469.135 Million cell updates/sec

Title: PEPI  
Perfect score: 690  
Sequence: 1 mdptapsralllllflhla.....rkmdrlsssglgckvlrrh 134

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 82229 seqs, 29864866 residues  
al number of hits satisfying chosen parameters: 82229

Minimum DB seq length: 0  
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database : SwissProt\_38.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	ID	Description
1	690	100.0	134	1	ANFB_HUMAN
2	334.5	48.5	131	1	ANFB_PIG
3	296	42.9	140	1	ANFB_CANFA
4	246.5	35.7	103	1	ANFB_BOVIN
5	171.5	24.9	121	1	ANFB_RAT
6	165.5	24.0	121	1	ANFB_MOUSE
7	137	19.9	140	1	ANFB_CHICK
8	118	17.1	149	1	ANFB_CANFA
9	113	16.4	152	1	ANFB_BOVIN
10	113	16.4	153	1	ANFB_HORSE
11	113	16.4	153	1	ANFB_HUMAN
12	109.5	15.9	150	1	ANFB_PIG
13	105.5	15.3	153	1	ANFB_RABIT
14	104	15.1	145	1	ANFB_CANFA
15	100	14.5	152	1	ANFB_MOUSE
16	97	14.1	152	1	ANFB_RAT
17	92.5	13.4	126	1	ANFB_BOVIN
18	92.5	13.4	126	1	ANFB_SHEEP
19	90.5	13.1	115	1	ANFB_CHICK
20	88	12.8	126	1	ANFB_PIG
21	87.5	12.7	126	1	ANFB_RAT
22	86.5	12.5	126	1	ANFB_HUMAN
23	86.5	12.5	135	1	ANFB_MOUSE
24	85.5	12.4	115	1	ANFB_MOUSE
25	85.5	12.4	126	1	ANFB_MOUSE
26	84	12.2	129	1	ANFB_MOUSE
27	83.5	12.0	131	1	ANFB_MOUSE
28	82.5	12.0	128	1	ANFB_MOUSE
29	81.5	11.8	118	1	ANFB_MOUSE
30	81	11.7	130	1	ANFB_MOUSE
31	80.5	11.7	1319	1	ANFB_MOUSE
32	77	11.2	36	1	ANFB_MOUSE
33	75.5	10.9	780	1	ANFB_MOUSE
34	74.5	10.8	780	1	ANFB_MOUSE

35	74	10.7	27	1	ANFB_MOUSE	P18144 anguilla ja
36	74	10.7	786	1	ANFB_MOUSE	O05319 drosophila
37	72	10.4	22	1	ANFB_MOUSE	P21805 gallus gall
38	72	10.4	271	1	ANFB_MOUSE	P15407 homo sapien
39	72	10.4	854	1	ANFB_MOUSE	O14721 homo sapien
40	71	10.3	615	1	ANFB_MOUSE	P46680 saccharomyc
41	71	10.3	1104	1	ANFB_MOUSE	O12986 homo sapien
42	70.5	10.2	662	1	ANFB_MOUSE	P53627 streptomyce
43	70	10.1	301	1	ANFB_MOUSE	P26596 lactococcus
44	70	10.1	853	1	ANFB_MOUSE	P15387 rattus norv
45	69	10.0	38	1	ANFB_MOUSE	P28374 dendroaspis

ALIGNMENTS

RESULT	ID	ANFB_HUMAN	STANDARD	PRT	134 AA.
AC	P16860	01-AUG-1990 (Rel. 15, Created)			
DT	01-AUG-1990 (Rel. 15, Last sequence update)				
DT	15-DEC-1998 (Rel. 37, Last annotation update)				
DE	BRAIN NATRIURETIC PEPTIDE PRECURSOR (BNP).				
GN	NPPB.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;				
OC	Eukaryota; Primates; Catarrhini; Hominoidea; Homo.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RP	MEDLINE: 90088474.				
RA	SETHAMER J.J., ARFSTEN A., MILLER J.A., LUNDQUIST P.,				
RA	SCARBOROUGH R.M., LEWICKI J.A., PORTER J.G.;				
RT	"Human and canine gene homologs of porcine brain natriuretic				
RT	peptide.";				
RL	Biochem. Biophys. Res. Commun. 165:650-658(1989).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RP	MEDLINE: 89193743.				
RA	SUDOH T., MAKIYAMA K., KOJIMA M., MINAMINO N., KANGAWA K., MATSUO H.;				
RT	"Cloning and sequence analysis of cDNA encoding a precursor for human				
RT	brain natriuretic peptide.";				
RL	Biochem. Biophys. Res. Commun. 159:1427-1434(1989).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RP	ERRINGTON H.;				
RL	Submitted (May-1998) to the EMBL/GenBank/DBJ databases.				
RN	[4]				
RP	SEQUENCE OF 27-58 AND 103-134.				
RA	HINO J., TATEYAMA H., MINAMINO N., KANGAWA K., MATSUO H.;				
RT	"Isolation and identification of human brain natriuretic peptides in				
RT	cardiac atrium.";				
RL	Biochem. Biophys. Res. Commun. 167:693-700(1990).				
RN	[5]				
RP	SEQUENCE OF 103-134.				
RP	MEDLINE: 90082577.				
RA	KABARASHI Y., NAKAO K., MUKOTAYAMA M., SAITO Y., OGAWA Y., SHONO S.;				
RT	"Isolation and sequence determination of human brain natriuretic				
RT	peptide in human atrium.";				
RL	FEBS Lett. 259:341-345(1990).				
CC	-1- FUNCTION: VASOACTIVE ACTIVITY.				
CC	-1- TISSUE SPECIFICITY: BRAIN AND ALSO IN ATRIA, BUT AT MUCH LOWER				
CC	LEVELS THAN ANP.				
CC	-1- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.				
CC	-----				
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RA ROY R.N,FLYNN T.G.;  
RT "Organization of the gene for iso-rANP, a rat B-type natriuretic  
RL peptide." Biochem. Res. Commun. 171:416-423(1990).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 92123224.  
RA DAGNINO L., DROUIN J., NEMER M.;  
RT "Differential expression of natriuretic peptide genes in cardiac and  
RL extracardiac tissues." Mol. Endocrinol. 5:1292-1300(1991).  
RN [4]  
RP SEQUENCE OF 27-121.  
RX MEDLINE; 89374230.  
RA ABUYARA M., HINO J., MINAMINO N., KANGAWA K., MATSUO H.;  
RT "Isolation and identification of rat brain natriuretic peptides in  
RL cardiac atrium." Res. Commun. 163:226-232(1989).  
RN [5]  
RP SEQUENCE OF 77-121.  
RC TISSUE=HEART;  
RX MEDLINE; 89374231.  
RA KAMAYASHI Y., ITOH H., HOSODA K., SAITO Y., YAMADA T.,  
RA MOTOYAMA M., ARAI H., SHIRAKAMI G., SUGA S.-I., OGAWA Y.,  
RA JOUGASAKI M., MINAMINO N., KANGAWA K., MATSUO H., INOUE K., IMURA H.;  
RT "Isolation and sequence determination of rat cardiac natriuretic  
RL peptide." Biochem. Biophys. Res. Commun. 163:233-240(1989).  
RN [6]  
RP SEQUENCE OF 77-121.  
RX MEDLINE; 89286593.  
RA FLINN T.G., BEAR A., TREMBLAY L., SANDA I., LYONS C., JENNINGS D.B.;  
RT "Isolation and Characterization of Iso-rANP, a new natriuretic  
RL peptide from rat atria." Biochem. Biophys. Res. Commun. 161:830-837(1989).  
RN [7]  
RP SEQUENCE OF 99-115.  
RX MEDLINE; 89286579.  
RA ITOH H., NAKAO K., KAMAYASHI Y., HOSODA K., SAITO Y., YAMADA T.,  
RA MOTOYAMA M., ARAI H., SHIRAKAMI G., SUGA S.-I., YOSHIDA I., INOUE K.,  
RA IMURA H.;  
RT "Occurrence of a novel cardiac natriuretic peptide in rats." Biochem. Biophys. Res. Commun. 161:732-739(1989).  
RN [8]  
RL FUNCTION: VASOACTIVE ACTIVITY.  
CC -1- TISSUE SPECIFICITY: BRAIN AND ALSO IN ATRIA, BUT AT MUCH LOWER LEVELS THAN ANP.  
CC -1- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.  
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CC -----  
DR EMBL; M25297; AAA57269.1; -;  
DR EMBL; M60731; AAA41456.1; -;  
DR EMBL; M60266; AAA41455.1; -;  
DR PIR; A30162; A30162.  
DR PIR; A32918; A32918.  
DR PIR; A32919; A32919.  
DR PIR; A33252; A33252.  
DR PIR; A33253; A33253.  
DR PIR; A35691; A35691.  
DR PROSITE; PS00263; NATRIURETIC-PEPTIDE; 1.  
DR PFAM; PF00212; ANP; 1.  
DR VASOACTIVE; Brain; Signal.  
FT SIGNAL 1 26  
FT PEPTIDE 27 121 GAMMA-BRAIN NATRIURETIC PEPTIDE.  
FT PEPTIDE 77 121 BRAIN NATRIURETIC PEPTIDE (5 KD CARDIAC  
FT PEPTIDE 99 115 NATRIURETIC PEPTIDE) (BNP-45).  
FT DISULFID 99 115

```

FT CONFLICT 15 15 L -> V (IN REF. 2) .
FT CONFLICT 120 120 L -> Q (IN REF. 6) .
SO SEQUENCE 121 AA; 13656 MW; 38EF466B CRC32;

Query Match 24.9%; Score 171.5; DB 1; Length 121;
Best Local Similarity 37.1%; Pred. No. 6.1e-10;
Matches 49; Conservative 18; Mismatches 52; Indels 13; Gaps 4;

OY 1 mddpqapsralllllllflhlafigrshp1gpgssasdlstg1gegrnh1gk1selye 60
Db 1 MDLQVLPQMLILFLFLWLSPLGGHSHPLGSPQSP--EGSTMQKLLILRKSEEMQR 58
OY 61 qtsleplqesprptgvtwksrevateg1gthpkmylyllrapsrpkwvsgscfg1kmdri 120
Db 59 Q-----LSKDGQPT-----KELLRKVLRSQSAFR1QRLL-RNSRMHASSSCFGQKIDRI 107
OY 121 ssssg1gckv1r 132
Db 108 GAVSR1GCDGLR 119

RESULT 6
ANFB_MOUSE STANDARD; PRT: 121 AA.
AC P40753;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE BRAIN NATRIURETIC PEPTIDE PRECURSOR (BNP).
GN NPBB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE=HEART;
RX MEDLINE; 94237953.
RA OGAWA Y., ITOH H., TAMURA N., SUGA S., YOSHIMASA T., UEHIRA M.,
RA MATSUDA S., SHIMO S., NISHIMOTO H., MAKAO K.;
RT "Molecular cloning of the complementary DNA and gene that encode
RT mouse brain natriuretic peptide and generation of transgenic mice
RT that overexpress the brain natriuretic peptide gene";
RL J. Clin. Invest. 93:1911-1921(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RX MEDLINE; 9328395.
RA STEINHELMER M.E.;
RT "Structure, expression, and genomic mapping of the mouse natriuretic
RT peptide type-B gene.";
RL Circ. Res. 72:984-992(1993).
CC -1- FUNCTION: ACTS AS A CARDIAC HORMONE WITH A VARIETY OF BIOLOGICAL
CC ACTIONS INCLUDING NATRIURESIS, DIURESIS, VASORELAXATION, AND
CC INHIBITION OF RENIN AND ALDOSTERONE SECRETION. IT IS THOUGHT TO
CC PLAY A KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS.
CC -1- ALTERNATIVE PRODUCTS: A SHORTER FORM (ONE AMINO ACID LESS) IS
CC GENERATED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: EXPRESSED ABUNDANTLY IN THE VENTRICLE, AND IN
CC A LESSER EXTENT IN THE ATRIUM.
CC -1- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
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CC -----
EMBL: D16497; BAA03948.1; -
EMBL: S58657; CAB31712.1; -
MGD: MGI:97368; NPBB.

```

[illegible]

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CC -----
DR EMBL: X57702; -; NOT_ANNOTATED_COS.
DR PIR: S14320; S14320.
DR PIR: A31509; A31509.
DR PROSITE: PS00263; NATRIURETIC-PEPTIDE; 1.
DR PFAM: PF00212; ANP; 1.
KW Vasoactive; Signal.
FT SIGNAL 1
FT PEPTIDE 112 140 ATRIAL NATRIURETIC PEPTIDE, ALPHA (ANP).
FT DISULFID 118 134
SQ SEQUENCE 140 AA; 15714 MW; E0A8F52F CRC32;

Query Match 19.9%; Score 137; DB 1; Length 140;
Best Local Similarity 29.9%; Pred. No. 1,5e-06;
Matches 43; Conservative 29; Mismatches 58; Indels 14; Gaps 4.

Oy 1 mdpgtapsrallllflflafgrshpispqgsasdlsglqegrhlgkls----- 56
Db 1 MDRSSFSFCGLFLLLTQLQ--PSANPYNLSPAKEL--ASMEALLELEDKFALTEAL 56
Oy 56 ----elqveqtsleplqgespptygwkar-ewategilghrkmvlytlrapspkmgqs 110
Db 57 ESNPLGEPQGEIPELTDDSDQKAPKASNTPLSRNPFLLKRLGVGMPRMARD 116
Oy 111 gcfgrkmgrlsssglgckvltirh 134
Db 117 GCFGRIRDRIGSLSGMGCSGRKN 140

RESULT 8
ANF_CANFA STANDARD: PRT: 149 AA.
AC P07499;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
DE (ANP) (PREPRONATRIOTIDILATIN).
GN NPFA.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Carnivora; Fissipedia; Canidae; Canis.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 86076957.
RA OKAWA S., IMAI M., INOZUKA C., TAMARAGI Y., NAKAZATO H., MATSUO H.;
RT "Structure of dog and rabbit precursors of atrial natriuretic
RT polypeptides deduced from nucleotide sequence of cloned cDNA.";
RL Biochem. Biophys. Res. Commun. 132:892-899(1985).
CC -1- FUNCTION: ATRIAL NATRIURETIC FACTOR (ANF) IS A POTENT VASOACTIVE
CC SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY A
CC KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A GMP-STIMULATING
CC ACTIVITY.
CC -1- MISCELLANEOUS: A DISULFIDE BOND IS REQUIRED FOR FULL ACTIVITY OF
CC ATRIOPEPTIN.
CC -1- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
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CC -----
DR EMBL: M12045; AAA30828.1; -.
DR PIR: A25302; AMDG.
DR PROSITE: PS00263; NATRIURETIC-PEPTIDE; 1.
DR PFAM: PF00212; ANP; 1.
KW Vasoactive; Signal.
FT SIGNAL 1
FT PEPTIDE 122 149 ATRIAL NATRIURETIC PEPTIDE, ALPHA (ANP).
FT DISULFID 122 149
SQ SEQUENCE 149 AA; 15714 MW; E0A8F52F CRC32;

```



```

OY 60 egtsleplgsesrpt-----gvyksrevategirghrkmvlyt-----lr 99
DB 70 ERALSLPEPEPTGVTGAVNPAQRGALGRGSDWS-----NSALKSKRLALLA 120
OY 100 apsrpkmgvsgcfcgkmdrlssssglgckvlyr 132
DB 121 APRS---LRSSCRGGRMDRIGAGSGLGCSNFR 150

RESULT 11
ANF_HUMAN STANDARD; PRT; 153 AA.
ID ANF_HUMAN
POL160:
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
DE (ANP) (PREPROMATRIODILATIN).
DE NPFA OR PND.
DE Homo sapiens (human).
DE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
DE Eutheria; Primates; Catarrhini; Hominiidae; Homo.
RN [1]
RX MEDLINE: 8421979.
RA OKAWA S., IMAI M., UENO A., TANAKA S., NOGUCHI T., NAKAZATO H.,
RA KANGAWA K., FUKUDA A., MATSUDO H.;
RT "Cloning and sequence analysis of cDNA encoding a precursor for human
RT atrial natriuretic polypeptide."
RL Nature 309:724-726(1984).
RN [2]
RP SEQUENCE OF 1-151 FROM N.A.
RX MEDLINE: 84295577.
RA NAKAYAMA K., OKUBO H., HIROSE T., INAYAMA S., NAKANISHI S.;
RT "mRNA sequence for human cardiolatin-atrial natriuretic factor
RT precursor and regulation of precursor mRNA in rat atria."
RL Nature 310:699-701(1984).
RN [3]
RP SEQUENCE OF 1-151 FROM N.A.
RX MEDLINE: 85061626.
RA NEMER M., CHAMBERLAND M., SIROIS D., ARGENTIN S., DROUIN J.,
RA DIXON R.A.F., ZIVIN R.A., COMDRA J.H.;
RT "Gene structure of human cardiac hormone precursor,
RT pronatriodilatin."
RL Nature 312:654-656(1984).
RN [4]
RP SEQUENCE OF 1-151 FROM N.A.
RX MEDLINE: 85061627.
RA GREENBERG B.D., BENGEN G.H., SEILHAMER J.J., LEWICKI J.A.,
RA FIDDES J.C.;
RT "Nucleotide sequence of the gene encoding human atrial natriuretic
RT factor precursor."
RL Nature 312:656-658(1984).
RN [5]
RP SEQUENCE OF 1-151 FROM N.A.
RX MEDLINE: 85065765.
RA SEIDMAN C.E., BLOCH K.D., KLEIN K.A., SMITH J.A., SEIDMAN J.G.;
RT "Nucleotide sequences of the human and mouse atrial natriuretic
RT factor genes."
RL Science 226:1206-1209(1984).
RN [6]
RP SEQUENCE OF 1-151 FROM N.A.
RA ERRINGTON H.;
RT Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE OF 118-153 FROM N.A.
RX MEDLINE: 85038509.
RA ZIVIN R.A., COMDRA J.H., DIXON R.A.F., SEIDMAN N.G., CHRETIEN M.,
RA NEMER M., CHAMBERLAND M., DROUIN J.;
RT "Molecular cloning and characterization of DNA sequences encoding rat
RT and human atrial natriuretic factors."
RL Proc. Natl. Acad. Sci. U.S.A. 81:6325-6329(1984).

```

```

RN [8]
RP SEQUENCE OF 1-75 FROM N.A.
RX MEDLINE: 85096983.
RA MAKI M., PARMENTIER M., INAGAMI T.;
RT "Cloning of genomic DNA for human atrial natriuretic factor."
RL Biochem. Biophys. Res. Commun. 125:797-802(1984).
RN [9]
RP SEQUENCE OF 124-151.
RX MEDLINE: 84128019.
RA KANGAWA K., MATSUDO H.;
RT "Purification and complete amino acid sequence of alpha-human atrial
RT natriuretic polypeptide (alpha-hANP)."
RL Biochem. Biophys. Res. Commun. 118:131-139(1984).
RN [10]
RP STRUCTURE BY NMR OF 124-151 MUTANT SELECTIVE FOR NPR-C RECEPTOR.
RX MEDLINE: 94318633.
RA FAIRBROTHER W.J., MCDOWELL R.S., CUNNINGHAM B.C.;
RT "solution conformation of an atrial natriuretic peptide variant
RT selective for the type A receptor."
RL Biochemistry 33:8897-8904(1994).
CC -1- FUNCTION: ATRIAL NATRIURETIC FACTOR (ANF) IS A POTENT VASOACTIVE
CC SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY A
CC KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A GMP-STIMULATING
CC ACTIVITY.
CC -1- MISCELLANEOUS: THE HUMAN GENOME CONTAINS 2 DIFFERENT
CC PREPROMATRIODILATIN GENES ONE CODES FOR 2 ARG RESIDUES AT THE
CC C-TERMINUS THAT ARE CLEAVED TO FORM THE MATURE PEPTIDE, WHILE THE
CC OTHER ENDS IN A TERMINATION CODON IMMEDIATELY AFTER THE LAST CODON
CC OF THE MATURE PEPTIDE.
CC -1- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
CC
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC
DR EMBL: X01470; CAA25699.1; -
DR EMBL: X02558; CAA25699.1; JOINED.
DR EMBL: K02043; AAB59379.1; -
DR EMBL: X01471; CAA25700.1; ALT_SEQ.
DR EMBL: K02044; AAA51730.1; -
DR EMBL: A021155; CAA15855.1; -
DR EMBL: M30262; AAA55668.1; -
DR EMBL: K02399; AAA35528.1; -
DR PIR: A01424; AMHU.
DR PIR: A22693; A22693.
DR PIR: A32733; A32733.
DR PDB: 1ANP; 07-APR-95.
DR MIM: 108780; -
DR PROSITE: PS00263; NATRIURETIC_PEPTIDE; 1.
DR PFAM: PF00212; ANP; 1.
KW Vasoactive; Signal; 3D-structure.
FT SIGNAL 1 25
FT PEPTIDE 26 55 CARDIOLATIN-RELATED PEPTIDE (CDP).
FT PEPTIDE 124 151 ATRIAL NATRIURETIC PEPTIDE, ALPHA (ANP).
FT DISULFID 130 146 BY SIMILARITY.
FT VARIANT 152 153 MISSING (IN ONE OF THE TWO GENES).
FT FTID-VAR 000594.
FT SEQUENCE 153 AA; 16708 MW; C24A68AF CRC32;

Query Match 16.4%; Score 113; DB 1; Length 153;
Best Local Similarity 30.7%; Pred. No. 0.00033;
Matches 47; Conservative 16; Mismatches 42; Indels 48; Gaps 8;

OY 14 lllfhaflg-grshlgspsasdlsglqgrhlgk-----lselqye 60
DB 12 LLLLAFLQLGQTRANPNYNAVSADL--MDFKLLDLHLKMPLEDEVPPQVLSPENE 69
OY 61 q-tsleplgsesrpt-----gvyksrevategirghrkmvlyt-----lr 99

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 27, 2000, 18:34:48 ; Search time 493.05 Seconds  
(without alignments)  
3078.424 Million cell updates/sec

Title: SEQ1  
Perfect score: 402  
Sequence: 1 atggtatcccccagacagcacc.....gcaagatgctgagcgccat 402

Scoring table: IDENTITY\_NUC  
Gapop 10.0 / Gapext 1.0

Searched: 4538634 seqs, 1887831982 residues  
1 number of hits satisfying chosen parameters: 9077268

Minimum DB seq length: 0  
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database :  
EST:\*  
1: em\_est1:\*  
2: em\_est2:\*  
3: em\_est3:\*  
4: em\_est4:\*  
5: em\_est5:\*  
6: em\_est6:\*  
7: em\_est7:\*  
8: em\_est8:\*  
9: em\_est9:\*  
10: em\_est10:\*  
11: em\_est11:\*  
12: em\_est12:\*  
13: em\_est13:\*  
14: em\_est14:\*  
15: em\_est15:\*  
16: em\_est16:\*  
17: em\_est17:\*  
18: em\_est18:\*  
19: em\_est19:\*  
20: gb\_est1:\*  
21: gb\_est2:\*  
22: gb\_est3:\*  
23: gb\_est4:\*  
24: gb\_est5:\*  
25: gb\_est6:\*  
26: gb\_est7:\*  
27: gb\_est8:\*  
28: gb\_est9:\*  
29: gb\_est10:\*  
30: gb\_est11:\*  
31: gb\_est12:\*  
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33: gb\_est14:\*  
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35: gb\_est16:\*  
36: gb\_est17:\*  
37: gb\_est18:\*  
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46: gb\_est27:\*  
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48: gb\_est29:\*  
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50: gb\_est31:\*  
51: gb\_est32:\*  
52: em\_est20:\*  
53: em\_est21:\*  
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64: gb\_est38:\*  
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71: gb\_est41:\*  
72: gb\_est42:\*  
73: gb\_est43:\*  
74: gb\_est44:\*  
75: em\_est31:\*  
76: em\_est32:\*  
77: em\_est33:\*  
78: em\_est34:\*  
79: gb\_gss1:\*  
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81: gb\_gss3:\*  
82: gb\_gss4:\*  
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84: em\_gss2:\*  
85: em\_gss3:\*  
86: em\_gss4:\*  
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88: gb\_gss6:\*  
89: gb\_gss7:\*  
90: gb\_gss8:\*  
91: gb\_gss9:\*  
92: em\_gss5:\*  
93: em\_gss6:\*  
94: em\_gss7:\*  
95: em\_gss8:\*  
96: em\_gss9:\*  
97: em\_gss10:\*  
98: em\_gss11:\*  
99: gb\_gss10:\*  
100: gb\_gss11:\*  
101: em\_gss12:\*  
102: gb\_gss12:\*  
103: gb\_gss13:\*  
104: gb\_gss14:\*  
105: gb\_gss15:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	287.6	71.5	360	30	AA216038	AA216038 hp0251.se
2	258.4	64.3	371	30	AA216138	AA216138 hp0519.se

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/organism="Homo sapiens"		
/db_xref="taxon:9606"		
/clone_id="Human fetal heart, Lambda ZAP Express"		
/lab_host="E. coli XL1-Blue"		
/note="Vector: Lambda ZAP Express; Site_1: EcoRI; Site_2: XhoI; mRNA was purified from human fetal hearts (8-10 weeks). cDNA was synthesized using a XhoI-Oligo dT adaptor-primer". EcoRI adaptors were ligated, followed by digestion with XhoI, for directional cloning into predigested Lambda ZAP Express."		
BASE COUNT	66 a	110 c 118 g 66 t
ORIGIN		
Query Match	71.5%	Score 287.6; DB 30; Length 360;
Best Local Similarity	94.7%	Prod. No. 2,3e-61;
Matches 341; Conservative	0; Mismatches 14; Indels 5; Gaps 4;	
QY	45	ctcttcgacatcgtgacattcctcgtggaagtcgctccca-ccgcgtggcagccccggttcag 103
Db	1	CTCTGTGGCGTCTGGCTTTCCTCGGAGGTCGTCTTACCCCCCTGGGAGCCCGGTTTCAG 60
QY	104	cctcggaacttggaaacgtccggtgttaagagagacgcgcaacacatttggagggcaaacatgt 163
Db	61	CCTCGGACTTGGAAACGTCGCGGTTACGAGGACGACGCAACATTGGAGGGCAAACTGT 120
QY	164	cggaggtctgcaggtgtgagacagacatccctg-gagccctccagagagagccccctgtccaca 222
Db	121	CGGAGCTGACAGTGGACACAGACATCCTGTGTAGGCCCTTCACGAGAGGCCCGCTGCCACA 180
QY	223	ggtgtc--tggaaagtcgccggaagtgaccacacgaaggacatcgtgtggcaccgcaaatgtg 280
Db	181	GGTGTGTGTGAAGTCCCGGAGGTACCCACCGAGGCGATCCGAGGGCACCGCAAAATGG 240
QY	281	tcctctaacacctcgggacacacgaagcccccaaga-tgtgtgcaaggtgtcgtgtctt 339
Db	241	TGCTCTACACCCCTTGGGACACAGAAAGCCCCCAAGATTGTGTGTCAAAGGCTTCGCTGCTTT 300



/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="Human fetal heart, Lambda ZAP Express"  
/lab\_host="E. coli XL1-Blue"  
/note="Vector: Lambda ZAP Express; Site-1: EcoRI; Site-2:  
XhoI; mRNA was purified from human fetal hearts (8-10  
weeks). cDNA was synthesized using a XhoI-0190 dr  
adaptor-primer. EcoRI adaptors were ligated, followed by  
digestion with XhoI, for directional cloning into  
predigested Lambda ZAP Express."

BASE COUNT 59 a 80 c 93 g 47 t

ORIGIN

Query Match 54.7%; Score 219.8; DB 30; Length 279;  
Best Local Similarity 98.1%; Pred. No. 9.9e-45;  
Matches 254; Conservative 0; Mismatches 2; Indels 3; Gaps 3;

146 attgagggcaaacgtgtcgagctgagctgagcagacatccctggagccctcagg 205  
|||||  
1 ATTTGAGGGCAAACTGTCTGAGCTGAGTGGAGCAGACATCCTGGAGCCCTCAGG 60  
|||  
QY 206 agagccccccgcccacaggtgtctggaagtcccggaagtgagccacgagggcatcgtg 265  
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DB 61 AGAGCCCCGCTCCACAGGAGTGTGGAGAGTCCGGAGAGTACGACGAGGCGATCCGTG 120  
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QY 266 ggcacggcaaaatggtctc-tacacctggtggagcaccagcagcagagatggtgcaa 324  
|||||  
DB 121 GGCACCGCAAAATAGTCTTACCTGACCTGGGGCACACGAAAGCCCAAGATGATACAA 180  
|||  
QY 325 gggctc-tgctgtcttggagagagatgagaccgatacagctcctcagtggtcgtgctg 383  
|||||  
DB 181 GGCTCTTGCTGCTTGGAGGAAGATGAGCAGATCAGCTCCTCCAGTGGCTGGGCTG 240  
|||  
QY 384 caaatgctgagggcgcat 402  
|||||  
DB 241 C-AAGTGTGAGGCGGCAT 258

RESULT 5  
AI634108/c 425 bp mRNA EST 26-APR-1999  
LOCUS wa88a04.x1 NCI-CGAP\_G66 Homo sapiens cDNA clone IMAGE:2303214 3'  
DEFINITION similar to gb:M25296 BRAIN NATURETIC PEPTIDE PRECURSOR (HUMAN);  
MRA sequence.  
ACCESSION AI634108  
VERSION AI634108.1 GI:4685438  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 425)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncigap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
On May 18, 1998 this sequence version replaced gi:3138182.  
Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert.Strausberg@nih.gov  
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael  
R. Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldi, Ph.D.  
cDNA library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/URL at:  
www.bio.lnl.gov/bhrp/image/image.html

JOURNAL  
COMMENT

Seq primer: -40UP from Gibco  
High quality sequence stop: 348.

FEATURES  
Source Location/Qualifiers  
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/lab\_host="DH10B"  
/note="Vector: pUT3D-Pac (Pharmacia) with a modified  
polylinker. Plasmid DNA from the normalized library  
in vitro. Following HAP purification, this DNA was used as  
tracer in a subtractive hybridization reaction. The driver  
was PCR-amplified cDNAs from a pool of 5,000 clones made  
from the same library (cloneIDs 1257096-1258631,  
146064-1470983, and 1475592-1476743). Subtraction by  
Bento Soares and M. Fatima Bonaldi."

BASE COUNT 114 a 109 c 103 g 97 t 2 others

ORIGIN

Query Match 46.7%; Score 187.8; DB 49; Length 425;  
Best Local Similarity 95.1%; Pred. No. 9e-37;  
Matches 214; Conservative 0; Mismatches 9; Indels 2; Gaps 2;

QY 178 ggcagacatccctgagacccctccagagagagcccgctccacaggtgtctgagatcc 237  
|||||  
DB 425 GAGCAGACATCTCTTGAGAGCCCTTCAGNAGAGCCCGCTCCACAGGTGTGNAAGTCC 366  
|||  
QY 238 cggaggtagccacccagggatccgtgtggcagcgcaaatgtctctaacacctg 297  
|||||  
DB 365 CGGAGGTAGCCACGAGAGGATCCGTGGGCACCAAAATGTCTCT-CACCTTGGCG 307  
|||  
QY 298 gaccacgaagcccaagatggtgcaaggtgtgtgtctgttggaggaagatggacgg 357  
|||||  
DB 306 GCACC-CGAAGCCCAAGATGTTGCAAGGTTGCTGCTTGGAGGAAGATGACCGG 248  
|||  
QY 358 atcagctcctccagtggtgctgcaaggtgtcgtgagcgcat 402  
|||||  
DB 247 ATCAGCTCTCTCCAGTGGCTGGCTGCAAAAGTGTGAGGCGGCAT 203

RESULT 6  
AA216210 228 bp mRNA EST 04-FEB-1997  
LOCUS hp0679.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens  
DEFINITION cdNA 5', mRNA sequence.  
ACCESSION AA216210  
VERSION AA216210.1 GI:1816149  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 228)  
Liew,C.C.  
cDNAs from fetal heart (1996)  
Unpublished (1996)  
On Sep 12, 1996 this sequence version replaced gi:1287882.  
Contact: Liew CC  
Department of Laboratory Medicine and Pathobiology  
University of Toronto  
Banting Institute, 100 College St., Toronto, Ontario, M5G1L5  
Tel: 4169788758  
Fax: 4169785650  
Email: liewc@utcc.utoronto.ca

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

FEATURES  
Source Location/Qualifiers  
1..228  
/organism="Homo sapiens"

PCR Primers  
FORWARD: 5' GCAGTGTGTAATTAACCTCACTAAGG 3'  
BACKWARD: 5' CCAATGATGTGATACGATCACTAATAGGCG 3'  
Seq primer: 5' GAATTAACCTCACTAAGG 3'.  
Location/Qualifiers  
1..228  
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/db\_xref="taxon:9606"  
/clone\_lib="Human fetal heart, lambda ZAP Express"  
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/note="Vector: Lambda ZAP Express; Site\_1: EcoRI; Site\_2:  
XhoI; mRNA was purified from human fetal hearts (8-10  
weeks). cDNA was synthesized using a XhoI-Oligo dt  
adaptor primer. EcoRI adaptors were ligated, followed by  
digestion with XhoI, for directional cloning into  
predigested lambda ZAP Express."

BASE COUNT 55 a 66 c 64 g 43 t  
ORIGIN

Query Match 39.8%; Score 160; DB 30; Length 228;  
Best Local Similarity 84.2%; Pred. No. 4.9e-30;  
Matches 192; Conservative 0; Mismatches 35; Indels 1; Gaps 1;

QY 160 ctctcgagctgacgtgagcagacatccctggagccctcgaagagagcccccctcc 219  
1 CTTGTGGAGCTCAGGTGAGCAGACATCCCTGGAGCCCTCAGAGAGCCCCCTCATC 60  
220 acaagctgtctgaagtcctggagagtagccacgagagcattcgtggagccgcaaaty 279  
Db 61 ACAGGTGCTGGAAGCTCCGGAGGAGGACGACGAGGCGCATTCGTGGCACCAGAAATG 120  
QY 280 gtcccttaacccctgagcagcagacagcccaagatgtgtcaagagctcgtgctt 339  
121 GTCCCTCAACACCTCGGGCAACCAAGAGCCCAAGATGTCACAAAGCTTGTCTT 179  
QY 340 gggaggaagatgacgcagctcctcagctgagctgagctgagctgagctgagct 387  
Db 180 TGGAGAGATGAGACCGATCACTCCATTCCTGCTGCTGCTGCTGCTGCTGCTGCT 227

RESULT 7  
A1968649/c 347 bp mRNA EST 25-AUG-1999  
LOCUS wt91b08.x1 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE:2514807 3'  
DEFINITION similar to gb:M25296 BRAIN NTR1URETIC PEPTIDE PRECURSOR  
(HUMAN); contains element PIR5 repetitive element; mRNA sequence.

ACCESSION A1968649 GI:5765467  
VERSION A1968649  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 347)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

JOURNAL Unpublished (1997)  
COMMENT On Jun 22, 1998 this sequence version replaced gi:3246732.  
Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550

REFERENCE Email: Robert.Strausberg@nih.gov  
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael  
R. Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www.bio.llnl.gov/bbrp/image/image.html

FEATURES  
Seq primer: -40UP from gibco  
High quality sequence stop: 344.  
Location/Qualifiers  
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/clone="IMAGE:2514807"

/clone\_lib="NCI CGAP GC6"  
/tissue\_type="pooled germ cell tumors"  
/lab\_host="DH10B"  
/note="Vector: pRT3D-Pac (Pharmacia) with a modified  
polylinker. Plasmid DNA from the normalized library  
NCI CGAP GC4 was prepared, and ss circles were made in  
vitro. Following HAP purification, this DNA was used as  
tracer in a subtractive hybridization reaction. The driver  
was PCR-amplified cDNAs from a pool of 5,000 clones made  
from the same library (clones 1257096-1258631,  
1469064-1470983, and 1475592-1476743). Subtraction by  
Bento Soares and M. Fatima Bonaldo."

BASE COUNT 99 a 85 c 83 g 80 t  
ORIGIN

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Best Local Similarity 98.0%; Pred. No. 4.6e-26;  
Matches 146; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 254 agggcatccgtggagcagcagcagcagcagcagcagcagcagcagcagcagcagc 313  
Db 343 AGTCCCTCGTGGGACCGCAAAATGCTCTACACCTCGGGCAGCAGACCCCA 284  
QY 314 agatgtcaagatgtcgtgcttggaggaagatgagccagctcagctcagctg 373  
Db 283 AGATGTGCAAGGCTGTGCTGCTTGGAGAGAGATGACCGGATCAGCTCTCAAGT 224  
QY 374 gcttggtgcaagatgtcgtgagcagcagcagcagcagcagcagcagcagcagc 402  
Db 223 GCCTGGCTGCAAAATGCTGAGCGCGCAT 195

RESULT 8  
A1186050/c 356 bp mRNA EST 09-OCT-1998  
LOCUS qe50q02.x1 Soares fetal lung, NBHL19W Homo sapiens cDNA clone  
IMAGE:1742450 3', similar to gb:M2526 BRAIN NTR1URETIC PEPTIDE  
PRECURSOR (HUMAN); mRNA sequence.

ACCESSION A1186050 GI:3736688  
VERSION A1186050  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 356)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550

REFERENCE Email: Robert.Strausberg@nih.gov  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Seq primer: -40UP from gibco.  
Location/Qualifiers  
1..356  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
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/dev\_stage="19 weeks"  
/lab\_host="DH10B (ampicillin resistant)"  
/note="Organ: lung; Vector: pRT3D (Pharmacia) with a  
modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer  
[5'-TGTTACCAATCTGAAGTGGAGGCGGCAATTTTITTTTITTTT-3'],  
double-stranded cDNA was size selected, ligated to Eco RI  
adapters (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of a modified pRT3D vector  
(Pharmacia). Library went through one round of

FEATURES  
source

normalization to a Cot = 5. Library constructed by Bento Soares and M. Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NBH19W."

BASE COUNT 98 a 83 c 79 g 96 t

Query Match 35.8%; Score 144; DB 43; Length 356;  
Best Local Similarity 100.0%; Pred. No. 5.2e-26;  
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 259 atccgtggacacgcgaatggtctctacacccctgcgggacgaagcccaaatg 318  
|||||  
DB 356 ATCCGTGGACACGCCAAATGCTCTACACCTCGCGGACACGACGACCAATG 297  
|||||  
QY 319 gtgcaaggctcgtgctcttggaggaagatgacgcgatacgtctccagtgcctg 378  
|||||  
296 GTGCAAGGCTCTGCGCTCTTGGAGGAAGATGACCGGATCAGCTCTCCAGTGCCTG 237  
|||||  
QY 379 ggtcgtcaaatgctgtagggcgcat 402  
|||||  
DB 236 GGCTGCAAGTCTGAGGCGGCAT 213  
|||||

RESULT 9 AA216011 333 bp mRNA EST 04-FEB-1997

LOCUS AA216011 hp0221.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens  
DEFINITION CDNA 5', mRNA sequence.  
ACCESSION AA216011  
VERSION AA216011.1 GI:1815966  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 333)  
AUTHORS IJew.C.C.  
TITLE CDNAs from fetal heart (1996)  
JOURNAL Unpublished (1996)  
COMMENT On Sep 12, 1996 this sequence version replaced gi:1324710.  
Contact: IJew CC  
Department of Laboratory Medicine and Pathobiology  
University of Toronto  
Banting Institute, 100 College St., Toronto, Ontario, M5G1L5  
Tel: 416/9788758  
Fax: 416/9785650  
Email: ijewc@utcc.utoronto.ca  
PCR PRIMERS  
FORWARD: 5' GCCAAGCTCGAATTACCTCACTAAGG 3'  
REVERSE: 5' CCAGTGAATGTAATGACGCTCACTAAGG 3'  
Seq primer: 5' GAATTACCTCACTAAGG 3'.  
Location/Qualifiers  
1. 333

FEATURES  
source  
1. 333  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="Human fetal heart, Lambda ZAP Express"  
/lab\_host="E. coli XL1-Blue"  
/note="Vector: Lambda ZAP Express; Site\_1: EcoRI; Site\_2: XhoI; mRNA was purified from human fetal hearts (8-10 weeks). CDNA was synthesized using a XhoI-Oligo dT adaptor-primer. EcoRI adaptors were ligated, followed by digestion with XhoI, for directional cloning into predigested Lambda ZAP Express."

BASE COUNT 83 a 77 c 86 g 87 t

Query Match 34.8%; Score 140; DB 30; Length 333;  
Best Local Similarity 99.3%; Pred. No. 4.8e-25;  
Matches 151; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 251 ccagggcatccgtgggacccgaatggtctctacacccctgcgggacccaagacc 310  
|||||

DB 1 CCAGGGCATCCGTGGGACCCGCAAAATGCTCTACACCTGCGGACCAAGGCC 59  
|||||

QY 311 ccaagatggtgcaagggtcgtgctcttggaggaagatgacgcgatacgtctcca 370  
|||||

DB 60 CCAAGATGCTGCAAGGCTCTGCTCTTGGAGGAAGATGACCGGATCAGCTCTCCA 119  
|||||

QY 371 gtgctggtcgtcgaagtgtcgtgtagggcgcat 402  
|||||  
DB 120 GTGCGCTGGGCTCAAAATGCTCTGAGCGGCAT 151  
|||||

RESULT 10 AI656014 296 bp mRNA EST 04-MAY-1999  
LOCUS AI656014/c t442e12.x1 NCI-CGAP\_G66 Homo sapiens CDNA clone IMAGE:2243470 3'  
DEFINITION similar to gb:M25296 BRAIN NATURETIC PEPTIDE PRECURSOR (HUMAN);  
mRNA sequence.  
ACCESSION AI656014 GI:4739993  
VERSION AI656014  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 296)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP).  
JOURNAL Tumor Gene Index  
COMMENT Unpublished (1997)  
On Jun 5, 1998 this sequence version replaced gi:3187756.  
Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert.Strausberg@nih.gov  
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.

CDNA library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
www.bio.llnl.gov/dbp/image/image.html

Seq primer: -40up from Gibco.  
Location/Qualifiers  
1. 296

FEATURES  
source  
1. 296  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_img="IMAGE:2243470"  
/clone\_lib="NCI-CGAP\_G66"  
/tissue\_type="pooled germ cell tumors"  
/lab\_host="DH10B"  
/note="Vector: pT773D-Pac (Pharmacia) with a modified polylinker. Plasmid DNA from the normalized library NCI-CGAP\_G64 was prepared, and ss circles were made in vitro. Following RAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonoids 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 91 a 72 c 59 g 74 t

Query Match 24.4%; Score 98; DB 49; Length 296;  
Best Local Similarity 100.0%; Pred. No. 1e-14;  
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 305 gaagcccaagatggtgcaagggtcgtgctcttggaggaagatgacgcgatacgt 364  
|||||



Db 296 GAAGCCCCAGATGTCAGAGGCTCTGCTCTTGGAGGAGATGACCGGATCAGCT 237  
QY 365 cctccagtgccctggctgcaaaagtctgtagggcgcat 402  
Db 236 CCTCAGTGGCTGGCTGGCTGCAAAAGTCTGAGGCGGCAAT 199

RESULT 11

AM197593 296 bp mRNA EST 29-NOV-1999  
LOCUS AM197593/c  
DEFINITION xnm44407.x1 NCI\_CGAP\_G6 Homo sapiens cDNA clone IMAGE:2687100 3'  
similar to gb:M25296 BRAIN NATRIURETIC PEPTIDE PRECURSOR (HUMAN);  
mRNA sequence.  
AM197593  
ACCESSION AM197593.1 GI:6476823  
VERSION  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutharia; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 296)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
On Jul 8, 1999 this sequence version replaced gi:5422539.  
Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert.Strausberg@nih.gov  
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael  
R. Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
www-bio.llnl.gov/dbp/image/image.html

JOURNAL COMMENT

Seq primer: -40UP from glibco.  
Location/Qualifiers  
1. .296  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_image="NCI\_CGAP\_G6"  
/clone\_lib="NCI\_CGAP\_G6"  
/issue\_type="pooled germ cell tumors"  
/lab\_host="DH10B"  
/note="Vector: PT73D-Pac (Pharmacia) with a modified  
polylinker; Plasmid DNA from the normalized library  
NCI-CGAP\_G6 was prepared and ss circles were made in  
vitro. Following HAP purification, this DNA was used as  
tracer in a subtractive hybridization reaction. The driver  
was PCR-amplified cDNAs from a pool of 5,000 clones made  
from the same library (clonoids 1257096-1258631,  
1469064-1470983, and 1475592-1476743). Subtraction by  
Bento Soares and M. Fatima Bonaldo."

FEATURES

source  
BASE COUNT 91 a 72 c 61 g 72 t  
ORIGIN

Query Match 24.4%; Score 98; DB 74; Length 296;  
Best Local Similarity 100.0%; Pred. No. 1e-14;  
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 305 gaagcccaagatggtgcaagagctgctgcttggaggaagatgacccgcatc 364  
Db 296 GAAGCCCCAGATGTCAGAGGCTCTGCTCTTGGAGGAGATGACCGGATCAGCT 237  
QY 365 cctccagtgccctggctgcaaaagtctgtagggcgcat 402  
Db 236 CCTCAGTGGCTGGCTGGCTGCAAAAGTCTGAGGCGGCAAT 199

RESULT 12  
AI656015 284 bp mRNA EST 04-MAY-1999  
LOCUS AI656015/c  
DEFINITION tt42f01.x1 NCI\_CGAP\_G6 Homo sapiens cDNA clone IMAGE:2243449 3'  
similar to gb:M25296 BRAIN NATRIURETIC PEPTIDE PRECURSOR (HUMAN);  
mRNA sequence.  
AI656015  
ACCESSION AI656015.1 GI:4739994  
VERSION  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutharia; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 284)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
On Jun 5, 1998 this sequence version replaced gi:3187757.  
Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert.Strausberg@nih.gov  
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael  
R. Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
www-bio.llnl.gov/dbp/image/image.html

Trace considered overall poor quality  
Seq primer: -40UP from glibco  
High quality sequence stop: 1.  
Location/Qualifiers  
1. .284  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_image="NCI\_CGAP\_G6"  
/clone\_lib="NCI\_CGAP\_G6"  
/issue\_type="pooled germ cell tumors"  
/lab\_host="DH10B"  
/note="Vector: PT73D-Pac (Pharmacia) with a modified  
polylinker; Plasmid DNA from the normalized library  
NCI-CGAP\_G6 was prepared and ss circles were made in  
vitro. Following HAP purification, this DNA was used as  
tracer in a subtractive hybridization reaction. The driver  
was PCR-amplified cDNAs from a pool of 5,000 clones made  
from the same library (clonoids 1257096-1258631,  
1469064-1470983, and 1473592-1476743). Subtraction by  
Bento Soares and M. Fatima Bonaldo."

JOURNAL COMMENT

Seq primer: -40UP from glibco  
Location/Qualifiers  
1. .284  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_image="NCI\_CGAP\_G6"  
/clone\_lib="NCI\_CGAP\_G6"  
/issue\_type="pooled germ cell tumors"  
/lab\_host="DH10B"  
/note="Vector: PT73D-Pac (Pharmacia) with a modified  
polylinker; Plasmid DNA from the normalized library  
NCI-CGAP\_G6 was prepared and ss circles were made in  
vitro. Following HAP purification, this DNA was used as  
tracer in a subtractive hybridization reaction. The driver  
was PCR-amplified cDNAs from a pool of 5,000 clones made  
from the same library (clonoids 1257096-1258631,  
1469064-1470983, and 1473592-1476743). Subtraction by  
Bento Soares and M. Fatima Bonaldo."

FEATURES

source  
BASE COUNT 96 a 70 c 59 g 59 t  
ORIGIN

Query Match 17.4%; Score 70; DB 49; Length 284;  
Best Local Similarity 84.0%; Pred. No. 8e-08;  
Matches 79; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 309 ccccaagatggtgcaagagctgctgcttggaggaagatgacccgcatc 368  
Db 280 CCCAATATGTGTGTCAGAGGCTCTGCTCTTGGAGGAGATGACCGGATCAGCT 221  
QY 369 cagtgccctggctgcaaaagtctgtagggcgcat 402  
Db 220 CAATGCATGGCTGCACAGTGTAGAGCGGCAAT 187  
RESULT 13  
LOCUS AA799914/c  
AA799914 337 bp mRNA EST 30-APR-1998





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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 27, 2000, 20:16:48 ; Search time 21.65 Seconds  
(without alignments)  
2223.035 Million cell updates/sec

Title: SEQ1  
Perfect score: 402  
Sequence: 1 atgataccccagacagcacc.....gcaagtcgtcagcgccat 402

Scoring table: IDENTITY\_NUC  
Gapop 10.0' , Gapext 1.0

Searched: 214294 seqs, 59861574 residues

Total number of hits satisfying chosen parameters: 428588

Minimum DB seq length: 0  
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
1: /cgn2\_6/ptodata/1/ina/5A.COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/5C.COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/5D.COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/6.COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/PTUS9.COMB.seq:\*  
7: /cgn2\_6/ptodata/1/ina/Backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	260.4	64.8	1519 4	US-08-850-910A-44 Sequence 44, Appl
2	182.2	45.3	707 4	US-08-850-910A-40 Sequence 40, Appl
3	139	34.6	1507 4	US-08-850-910A-38 Sequence 38, Appl
4	123.8	30.8	1504 4	US-08-850-910A-17 Sequence 17, Appl
5	116.4	29.0	1804 4	US-08-850-910A-42 Sequence 42, Appl
6	39.8	9.9	1926 1	US-08-278-728A-22 Sequence 22, Appl
7	39.8	9.9	1926 1	US-08-480-528A-9 Sequence 9, Appl
8	39.8	9.9	1926 2	US-08-643-563A-22 Sequence 22, Appl
9	39.8	9.9	1926 2	US-08-643-763A-22 Sequence 22, Appl
10	39.8	9.9	1926 2	US-08-462-623-22 Sequence 22, Appl
11	39.8	9.9	1926 2	US-08-451-953A-22 Sequence 22, Appl
12	39.8	9.9	1926 3	US-08-445-458A-22 Sequence 22, Appl
13	39.8	9.9	1926 4	US-08-461-397A-22 Sequence 22, Appl
14	39.8	9.9	1926 4	US-08-912-088-22 Sequence 22, Appl
15	38.2	9.5	1926 1	US-07-901-703-12 Sequence 12, Appl
16	38.2	9.5	1926 1	US-08-147-023-26 Sequence 26, Appl
17	38.2	9.5	1926 1	US-08-479-666-9 Sequence 9, Appl
18	38.2	9.5	1926 1	US-08-155-343A-22 Sequence 22, Appl
19	38.2	9.5	1926 1	US-08-406-672-22 Sequence 22, Appl
20	38.2	9.5	1926 2	US-08-447-570-26 Sequence 26, Appl
21	38.2	9.5	1926 3	US-08-459-346-7 Sequence 7, Appl
22	38.2	9.5	1926 3	US-08-901-200A-9 Sequence 9, Appl
23	38.2	9.5	1926 3	US-08-449-700-26 Sequence 26, Appl
24	38.2	9.5	1926 6	US-08-449-699A-26 Sequence 26, Appl
25	38.2	9.5	1926 6	PCT-US92-01968-22 Sequence 12, Appl
26	38.2	9.5	1926 6	PCT-US93-05446-12 Sequence 12, Appl
27	38.2	9.5	1926 6	PCT-US93-07189-7 Sequence 7, Appl

c 28	38.2	9.5	1926 6	PCT-US93-07190-22	Sequence 22, Appl
c 29	38.2	9.5	1926 6	PCT-US93-07231-22	Sequence 22, Appl
c 30	38.2	9.5	1926 6	PCT-US93-08742-22	Sequence 22, Appl
c 31	38.2	9.5	1926 6	PCT-US93-08808-22	Sequence 22, Appl
c 32	38.2	9.5	1926 6	PCT-US93-08885-22	Sequence 22, Appl
c 33	38.2	9.5	1926 6	PCT-US93-10520-9	Sequence 9, Appl
c 34	37.4	9.3	806 7	5212286-5	Patent No. 5212286
c 35	34.8	8.7	2589 7	5212286-1	Patent No. 5212286
c 36	34.6	8.6	378 4	US-07-757-606B-2	Sequence 2, Appl
c 37	34.6	8.6	434 4	US-07-757-606B-5	Sequence 5, Appl
c 38	34.6	8.6	549 1	US-07-728-221B-12	Sequence 12, Appl
c 39	34.6	8.6	1020 4	US-07-757-606B-3	Sequence 3, Appl
c 40	34.6	8.6	1020 4	US-07-757-606B-7	Sequence 7, Appl
c 41	34.2	8.5	3252 4	US-08-809-740A-1	Sequence 1, Appl
c 42	34.2	8.5	3252 4	US-08-809-740A-4	Sequence 4, Appl
c 43	33.6	8.4	1313 2	US-08-176-427B-7	Sequence 7, Appl
c 44	33.6	8.4	1313 3	US-08-356-060A-4	Sequence 4, Appl
c 45	33.6	8.4	1843 2	US-08-499-523-9	Sequence 9, Appl

## ALIGNMENTS

RESULT 1  
US-08-850-910A-44  
Sequence 44, Application US/08850910A  
Patent No. 5948761  
GENERAL INFORMATION:  
APPLICANT: SELHAMER, J.J.  
APPLICANT: LEWICKI, J.  
APPLICANT: SCARBOROUGH, R.M.  
TITLE OF INVENTION: RECOMBINANT TECHNIQUES FOR  
PRODUCTION OF BRAIN NERVE TISSUE PEPTIDE  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER, LLP  
STREET: 2000 Pennsylvania Avenue, NW, Suite 5500  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20006-1868  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FASTSEQ for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/850, 910A  
FILING DATE: 05-MAY-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/477, 226  
FILING DATE: 08-FEB-1990  
APPLICATION NUMBER: 07/299, 880  
FILING DATE: 19-JAN-1989  
APPLICATION NUMBER: 07/206, 470  
FILING DATE: 14-JUN-1988  
APPLICATION NUMBER: 07/200, 383  
FILING DATE: 31-MAY-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Murashige, Kate H  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 219002025212  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-867-1500  
TELEFAX: 202-822-0168  
TELEX:  
INFORMATION FOR SEQ ID NO: 44:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1519 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear





Dh 645 CCCAGACGATGCGTGCCTGCTTGGCGAGAGCTGACCGATGCGCTCCCTC 704  
QY 370 atgagcctggctgctgcaag 388  
|||  
Dh 705 AGCGGCTGGGCTGCATG 723

## RESULT 5

US-08-850-910A-42  
Sequence 42, Application US/08850910A  
Patent No. 5948761  
GENERAL INFORMATION:  
APPLICANT: SEILHAMER, J.J.  
APPLICANT: LEWICKI, J.  
APPLICANT: SCARBOROUGH, R.M.  
TITLE OF INVENTION: RECOMBINANT TECHNIQUES FOR  
TITLE OF INVENTION: PRODUCTION OF BRAIN NUTRIENTIC PEPTIDE  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: MORRISON & FOERSTER, LLP  
STREET: 2000 Pennsylvania Avenue, NW, Suite 5500  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20006-1888  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FASTSEQ for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/850,910A  
FILING DATE: 05-MAY-1997  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/477,226  
FILING DATE: 08-FEB-1990  
APPLICATION NUMBER: 07/239,880  
FILING DATE: 19-JAN-1989  
APPLICATION NUMBER: 07/206,470  
FILING DATE: 14-JUN-1988  
APPLICATION NUMBER: 07/200,383  
FILING DATE: 31-MAY-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Murashige, Kate H  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 219002025212  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-887-1500  
TELEFAX: 202-822-0168  
TELEX:  
INFORMATION FOR SEQ ID NO: 42:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1804 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 365...490  
OTHER INFORMATION:  
NAME/KEY: CDS  
LOCATION: 740...791  
OTHER INFORMATION:  
NAME/KEY: CDS  
LOCATION: 1558...1569  
OTHER INFORMATION:  
US-08-850-910A-42

Query Match 29.0%; Score 116.4; DB 4; Length 1804;  
Best Local Similarity 67.9%; Pred. No. 9.9e-23;  
Matches 178; Conservative 0; Mismatches 81; Indels 3; Gaps 1;

QY 127 ttacagagcagcgcaaccatttgcagggcaactgtcgagctgaggtggagcagaca 186  
|||  
Dh 734 TTGCAGAGACTGCTGGGCGCTGTGAAGAGCGAGTTTCAGACTGCGAGCAGCAGTG 793  
|||  
QY 187 tccctgagagccctccagagagagcccgctcccaagagtgtctgaaagtcgggaagta 246  
|||  
Dh 794 GCCCTGAACCCCTGCACGAGCCACAGCCCGCGAGAGCCCGGAGGCGC--GGAGGA 850  
|||  
QY 247 gccaccgagggcatcgctgagcagcgaatggtctctacagcctgaggcagcaga 306  
|||  
Dh 851 AGCCCGGTGGGCTCTTGCACCCATGACAGTGTCTCAGGCGCTGAGAAAGACTACCC 910  
|||  
QY 307 agccccaagatggtgcaaggtcgtgctgttgaggaggaagatgaccgcagtcac 366  
|||  
Dh 911 AGCCCAAGTATGATGCAAGTCAGAGGTCTTGGCGGAGGCTGACCGATCGGCTCC 970  
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QY 367 tccagtggcctggctgcaag 388  
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Dh 971 CTCAGTGGCCTGGGCTGCATG 992

## RESULT 6

US-08-278-729A-22/c  
Sequence 22, Application US/08278729A  
Patent No. 5650276  
GENERAL INFORMATION:  
APPLICANT: SMART, JOHN  
APPLICANT: OPPERMAN, HERMAN  
APPLICANT: OKAMURA, ENGIN  
APPLICANT: KUBERASAMPATH, THANGAVEL  
APPLICANT: RUEGER, DAVID C.  
APPLICANT: PANG, ROY H. L.  
APPLICANT: COHEN, CHARLES M.  
TITLE OF INVENTION: MORPHOGENIC PROTEIN SCREENING METHOD  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES  
STREET: 45 SOUTH STREET  
CITY: HOPKINTON  
STATE: MA  
COUNTRY: USA  
ZIP: 01748  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/278,729A  
FILING DATE: 20-JUL-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: PITCHER Esq., EDMUND R.  
REGISTRATION NUMBER: 27,829  
REFERENCE/DOCKET NUMBER: CRP-058CPTW  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (508) 435-9001  
TELEFAX: (508) 435-6951  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1926 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 93...1289  
OTHER INFORMATION: /Product= "MOP2 CDNA"  
US-08-278-729A-22



Query Match 9.9%; Score 39.8; DB 1; Length 1926;  
Best Local Similarity 47.9%; Pred. No. 0.033;  
Matches 145; Conservative 0; Mismatches 157; Indels 1; Gaps 1;

QY 66 gggaggtcgtcccaaccgctggcagcccggttcagcctcgacttgaacgtccg 125  
DB 312 GGGGCGGAGCGCTGCTCGGGGACCGCGGCTGTGACACGGGGTCCGCCG 253

QY 126 gtacagagacagcagcaaccatttgcagggcaacttcgagctgcaagtgcagcagac 185  
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QY 186 atccctggagcccccaccagagagcccccgctcccaagtgctggaagtcgccggag-g 244  
DB 192 GAGGCTGGGACAGGTGTGGGGGAGCGGACCGCTGCGCCCTCCACGCGCAGAG 133

QY 245 tagccaccgagggcagtcgctggcagccgcaaaatgctctctacacccctgcggaccac 304  
DB 132 CAAGGCCCAATAGCAGAGTGGCCCGGAGCATAGCCATCTCGACTTCAGCGCGC 73

DB 305 gaagccccaagatggtcgaaggtctgctgcttggaggaagatgacccgatacgt 364  
DB 72 GCATCCACTGTAGCTGTGCTGGCTCGCTGACGCCAGACGGGAGAGACAGCGCGCA 13

QY 365 cct 367  
DB 12 CCT 10

RESULT 7

US-08-480-528A-9/C

Sequence 9, Application US/08480528A

Patent No. 5652118

GENERAL INFORMATION:

APPLICANT: OPPERMAN, HERMAN

APPLICANT: OZKAYNAK, ENGIN

APPLICANT: KUBERASAMPATH, THANGAVEL

APPLICANT: RUEGER, DAVID C.

APPLICANT: PANG, ROY H. L.

APPLICANT: COHEN, CHARLES M.

TITLE OF INVENTION: OP3-INDUCED MORPHOGENESIS

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESSES:

ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES

STREET: 45 SOUTH STREET

CITY: HOPKINTON

STATE: MA

COUNTRY: USA

ZIP: 01748

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/480,528A

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: FENTON Esq., GILLIAN M.

REGISTRATION NUMBER: 36,508

REFERENCE/DOCKET NUMBER: CRP-076FW

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 248-7560

TELEFAX: (617) 248-7100

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 1926 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS  
LOCATION: 93..1289  
OTHER INFORMATION: /function="OSTEOGENIC PROTEIN"  
OTHER INFORMATION: /product="MOP2-PP"  
OTHER INFORMATION: /note="MOP2 cDNA"

US-08-480-528A-9  
Query Match 9.9%; Score 39.8; DB 1; Length 1926;  
Best Local Similarity 47.9%; Pred. No. 0.033;  
Matches 145; Conservative 0; Mismatches 157; Indels 1; Gaps 1;

QY 66 gggaggtcgtcccaaccgctggcagcccggttcagcctcgacttgaacgtccg 125  
DB 312 GGGGCGGAGCGCTGCTCGGGGACCGCGGCTGTGACACGGGGTCCGCCG 253

QY 126 gtacagagacagcagcaaccatttgcagggcaacttcgagctgcaagtgcagcagac 185  
DB 252 GTAGCCCGACCGCCAGGATTTACGCTGATGCGCGGCTCCCGCGCTCCAGGC 193

QY 186 atccctggagcccccaccagagagcccccgctcccaagtgctggaagtcgccggag-g 244  
DB 192 GAGGCTGGGACAGGTGTGGGGGAGCGGACCGCTGCGCCCTCCACGCGCAGAG 133

QY 245 tagccaccgagggcagtcgctggcagccgcaaaatgctctctacacccctgcggaccac 304  
DB 132 CAAGGCCCAATAGCAGAGTGGCCCGGAGCATAGCCATCTCGACTTCAGCGCGC 73

QY 305 gaagccccaagatggtcgaaggtctgctgcttggaggaagatgacccgatacgt 364  
DB 72 GCATCCACTGTAGCTGTGCTGGCTCGCTGACGCCAGACGGGAGAGACAGCGCGCA 13

QY 365 cct 367  
DB 12 CCT 10

RESULT 8

US-08-643-563A-22/C

Sequence 22, Application US/08643563A

Patent No. 5707810

GENERAL INFORMATION:

APPLICANT: SMART, JOHN

APPLICANT: OPPERMAN, HERMAN

APPLICANT: OZKAYNAK, ENGIN

APPLICANT: KUBERASAMPATH, THANGAVEL

APPLICANT: RUEGER, DAVID C.

APPLICANT: PANG, ROY H. L.

APPLICANT: COHEN, CHARLES M.

TITLE OF INVENTION: MORPHOGENIC PROTEIN SCREENING METHOD

NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESSES:

ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES

STREET: 45 SOUTH STREET

CITY: HOPKINTON

STATE: MA

COUNTRY: USA

ZIP: 01748

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/643,563A

FILING DATE: 06-MAY-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: TWOMEY Esq., MICHAEL J.

REGISTRATION NUMBER: 38,349

REFERENCE/DOCKET NUMBER: CRP-058CN2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (508) 435-9001



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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,623
FILING DATE:
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/445,882
FILING DATE: 22-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: FENTON ESQ., GILLIAN M.
REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: CRP-074CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 435-9001
TELEFAX: (508) 435-6951
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 1926 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 93..1289
OTHER INFORMATION: /product= "MOP2 CDNA"
US-08-462-623-22
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Query Match          9.9%; Score 39.8; DB 2; Length 1926;
Best Local Similarity 47.9%; Pred. No. 0.033;
Matches 145; Conservative 0; Mismatches 157; Indels 1; Gaps 1;

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DB 312 gggggcggagacctgctgctccggcgacggcggtgtgacaggggtccggcgccg 253

QY 126 gttaagagcagcagcaaccttgcagggcaactgtcggagctgcaggttgagcagac 185
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DB 252 gtaccccgacacgacgacgatttcacgtgcatgtcggcgctgcgctccacagcg 193

QY 186 atccctggagccctccagagagagcccgctcccaagtgctggaagtcccgagag-g 244
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DB 192 gacgctggggagacagtgctgcccgggagcggcagccgtgcccctccacgacagag 133

QY 245 tagcaccagggagcgtcgttggcagccgcaaatgtctctacacccctggcgagcagc 304
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DB 132 CAAGGCCCAATAGCCAGATGGCCCGGAGCAGCATCTCGGACTTTCAGCCGGCCG 73

QY 305 gaagcccaagatgtgcaaggtctgctgtcttgggaggaagatygaccgagtcagct 364
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DB 72 GCATCAGCTGTGAGCTGTGCTGGGCTCGGTGACGCCAGACGGGAGAGACCAAGCGCGCA 13

QY 365 cct 367
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DB 12 cct 10
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RESULT 11
US-08-451-953A-22/c
; Sequence 22, Application US/08451953A
; Patent No. 5741641
; GENERAL INFORMATION:
; APPLICANT: SMART, JOHN
; APPLICANT: OPPERMAN, HERMAN
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: ROEGER, DAVID C.
; APPLICANT: PANG, ROY H.L.
```

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APPLICANT: COHEN, CHARLES M.
TITLE OF INVENTION: MORPHOGENIC PROTEIN SCREENING METHOD
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESS: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
STREET: 45 SOUTH STREET
CITY: HOPKINTON
STATE: MA
COUNTRY: USA
ZIP: 01748
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,953A
FILING DATE: 26-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ., EDMUND R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-058CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 435-9001
TELEFAX: (508) 435-6951
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 1926 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 93..1289
OTHER INFORMATION: /product= "MOP2 CDNA"
US-08-451-953A-22
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Query Match          9.9%; Score 39.8; DB 2; Length 1926;
Best Local Similarity 47.9%; Pred. No. 0.033;
Matches 145; Conservative 0; Mismatches 157; Indels 1; Gaps 1;

QY 66 gggaggtcgtccaccctcgtggcagcccggttcagcctcggaacttgaaagtcg 125
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 312 gggggcggagacctgctgctccggcgacggcggtgtgacaggggtccggcgccg 253

QY 126 gttaagagcagcagcaaccttgcagggcaactgtcggagctgcaggttgagcagac 185
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DB 252 gtaccccgacacgacgacgatttcacgtgcatgtcggcgctgcgctccacagcg 193

QY 186 atccctggagccctccagagagagcccgctcccaagtgctggaagtcccgagag-g 244
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QY 245 tagcaccagggagcgtcgttggcagccgcaaatgtctctacacccctggcgagcagc 304
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DB 132 CAAGGCCCAATAGCCAGATGGCCCGGAGCAGCATCTCGGACTTTCAGCCGGCGC 73

QY 305 gaagcccaagatgtgcaaggtctgctgtcttgggaggaagatygaccgagtcagct 364
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DB 72 GCATCAGCTGTGAGCTGTGCTGGGCTCGGTGACGCCAGACGGGAGAGACCAAGCGCGCA 13

QY 365 cct 367
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DB 12 cct 10
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RESULT 12
US-08-445-468A-22/c
; Sequence 22, Application US/08445468A
; Patent No. 5849686
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Best Local Similarity 47.5%; Pred. No. 0.09;  
Matches 144; Conservative 0; Mismatches 158; Indels 1; Gaps 1;

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Db 312 GGGGCGCGGACGCTGGCTGCCGGGACGCGGGTTGTGCACGGGGTCGGGGCGCTCCG 253
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QY 126 gtacagagagcagcgaaccattgcagggcaactgtcgagctgcaggtgagcagac 185
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Db 252 GTAGCCCGAGACCGCCAGGATTTCACAGCTGCATGTCGGCGCTCGCGGCTCCAGGC 193
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QY 186 atccctggaagccccctcagagagagccccgtcccaaggtgtctggaagtcgccggag-9 244
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Db 192 GACGCTGGGGACAGGTGTGTGGGGGAGCGGACCGTGGCCGCTCCAGCGCGCACAGAG 133
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QY 245 tagcaacgagggcatccgttgggcacccgcaaaatgtctctacaacctgcgggcaaac 304
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    132 CAAGGCCCAATAGCCAGAGTGGCCCGGAGCAGCATAGCCATCTCGACTTTCAGCGCGGC 73
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    305 gaagccccaagatggtgcagaggtctggtctgtcttgggaagatggaaccggaatcagct 364
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Db 72 GCATCCACTGGTAGCTGTGGCTCGGCTGACGCCAGACGGGAGGACCAAGCGGCGCA 13
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QY 365 cct 367
    |||
Db 12 CCT 10

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Job time: 14557 sec

Mon May 1 10:09:25 2000

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Page 1

GenCore version 4.5  
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OM protein - protein search, using sw model

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Perfect score: 690  
Sequence: 1 mppqtapsrallllllflhla.....rkmdrlssssgkylrrh 134

Scoring table: BLOSUM62  
Gapop 10.0 , Gapept 0.5

Searched: 133990 seqs, 13297546 residues

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Post-processing: Minimum Match 0%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	690	100.0	134 2 US-08-850-910A-48	Sequence 48, Appl
2	677	98.1	134 2 US-08-850-910A-45	Sequence 45, Appl
3	392	56.8	76 1 US-08-338-358-1	Sequence 1, Appl
4	334.5	48.5	131 2 US-08-850-910A-39	Sequence 39, Appl
5	334.5	48.5	131 2 US-08-850-910A-41	Sequence 41, Appl
6	334.5	48.5	131 2 US-08-850-910A-46	Sequence 46, Appl
7	307	44.5	132 2 US-08-850-910A-47	Sequence 47, Appl
8	289.5	42.0	131 2 US-08-850-910A-43	Sequence 43, Appl
9	202	29.3	106 2 US-08-850-910A-30	Sequence 30, Appl
10	169	24.5	32 1 US-07-828-450-41	Sequence 41, Appl
11	169	24.5	32 1 US-08-297-330-2	Sequence 2, Appl
12	169	24.5	32 1 US-08-451-240-22	Sequence 22, Appl
13	169	24.5	32 2 US-08-470-846A-3	Sequence 3, Appl
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15	169	24.5	32 2 PCT-US94-12591-22	Sequence 22, Appl
16	158	22.9	32 1 US-08-451-240-3	Sequence 3, Appl
17	158	22.9	32 1 PCT-US94-12591-3	Sequence 3, Appl
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20	122	17.7	32 1 US-07-754-947-5	Sequence 5, Appl
21	113	16.4	125 2 US-08-862-480B-1	Sequence 1, Appl
22	113	16.4	151 5 5212286-2	Sequence 18, Appl
23	108.5	15.7	177 2 US-08-850-910A-18	Sequence 18, Appl
24	106.5	15.4	136 5 5212286-4	Sequence 3, Appl
25	106	15.4	26 1 US-07-778-847-2	Sequence 2, Appl
26	106	15.4	26 2 US-08-850-910A-3	Sequence 3, Appl
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29	97	14.1	152 5 5212286-6	Sequence 4, Appl

30	92	13.3	29 1 US-07-754-958-6	Sequence 6, Appl
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34	87	12.6	32 1 US-08-451-240-2	Sequence 2, Appl
35	87	12.6	32 1 US-08-737-927-4	Sequence 4, Appl
36	87	12.6	32 2 US-08-470-846A-18	Sequence 18, Appl
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38	87	12.6	32 5 5449751-1	Sequence No. 5449751
39	87	12.6	32 5 5449751-3	Sequence No. 5449751
40	86	12.5	20 2 US-08-850-910A-34	Sequence 34, Appl
41	82	11.9	22 1 US-07-828-450-10	Sequence 10, Appl
42	82	11.9	22 1 US-07-828-450-13	Sequence 13, Appl
43	82	11.9	27 1 US-07-828-450-5	Sequence 5, Appl
44	82	11.9	27 1 US-08-297-330-4	Sequence 4, Appl
45	82	11.9	27 4 PCT-US94-02391-4	Sequence 4, Appl

#### ALIGNMENTS

RESULT 1  
US-08-850-910A-48  
Sequence 48, Application US/08850910A  
Patent No. 5948761  
GENERAL INFORMATION:  
APPLICANT: SEILAMER, J.J.  
APPLICANT: LEWICKI, J.  
APPLICANT: SCARBOROUGH, R.M.  
TITLE OF INVENTION: RECOMBINANT TECHNIQUES FOR  
PRODUCTION OF BRAIN NUTRIENT PEPTIDE  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER, LLP  
STREET: 2000 Pennsylvania Avenue, NW, Suite 5500  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20006-1888  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FASTSEQ for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/850,910A  
FILING DATE: 05-MAY-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/477,226  
FILING DATE: 08-FEB-1990  
APPLICATION NUMBER: 07/299,880  
FILING DATE: 19-JAN-1989  
APPLICATION NUMBER: 07/206,470  
FILING DATE: 14-JUN-1988  
APPLICATION NUMBER: 07/200,383  
FILING DATE: 31-MAY-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Murashige, Kate H  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 219002025212  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-887-1500  
TELEFAX: 202-822-0168  
TELEX:  
INFORMATION FOR SEQ ID NO: 48:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 134 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-850-910A-48





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US-08-850-910A-39
: Sequence 39, Application US/08850910A
: Patent No. 5948761
: GENERAL INFORMATION:
: APPLICANT: SEILHAMER, J.J.
: APPLICANT: LEWICKI, J.
: APPLICANT: SCARBOROUGH, R.M.
: TITLE OF INVENTION: RECOMBINANT TECHNIQUES FOR
: TITLE OF INVENTION: PRODUCTION OF BRAIN NATRIURETIC PEPTIDE
: NUMBER OF SEQUENCES: 50
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MORRISON & FOERSTER, LLP
: STREET: 2000 Pennsylvania Avenue, NW, Suite 5500
: CITY: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20006-1888
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: Windows
: SOFTWARE: FastSeq for Windows Version 2.0b
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/850,910A
: FILING DATE: 05-MAY-1997
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/477,226
: FILING DATE: 08-FEB-1990
: APPLICATION NUMBER: 07/299,880
: FILING DATE: 19-JAN-1989
: APPLICATION NUMBER: 07/206,470
: FILING DATE: 14-JUN-1988
: APPLICATION NUMBER: 07/200,383
: FILING DATE: 31-MAY-1988
: ATTORNEY/AGENT INFORMATION:
: NAME: Murashige, Kate H
: REGISTRATION NUMBER: 29,959
: REFERENCE/DOCKET NUMBER: 219002025212
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-867-1500
: TELEFAX: 202-822-0168
: TELEX:
: INFORMATION FOR SEQ ID NO: 39:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 131 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: FRAGMENT TYPE: internal
: US-08-850-910A-39

Query Match      48.5%; Score 334.5; DB 2; Length 131;
Best Local Similarity 53.0%; Pred. No. 8.9e-31;
Matches 71; Conservative 20; Mismatches 40; Indels 3; Gaps 2;

QY 1 mdpqtapsra1111f1h1a1fgrshp1gspgsasdltsq1gqgrnh1gk1se1qve 60
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 1 MGPMAAPR-VLLLFLLFLILGCRSHPLGGAGLASEL--PGIOELDLRLDRVSELOAE 57

QY 61 qtslepdgsprptgvykswrevateg1gghkmylytlraprpskmyvgsgcfcgrkndr1 120
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 58 RTDLEPLRQDGLTEANEARAAAPTVGLGPRSSIFQVLRGIRSPKTMDSGCFGRRLDRI 117

QY 121 ssssg1gckv1lrh 134
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 118 GSLSGLCGNVLRRY 131

RESULT 5
US-08-850-910A-41

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```

: Sequence 41, Application US/08850910A
: Patent No. 5948761
: GENERAL INFORMATION:
: APPLICANT: SEILHAMER, J.J.
: APPLICANT: LEWICKI, J.
: APPLICANT: SCARBOROUGH, R.M.
: TITLE OF INVENTION: RECOMBINANT TECHNIQUES FOR
: TITLE OF INVENTION: PRODUCTION OF BRAIN NATRIURETIC PEPTIDE
: NUMBER OF SEQUENCES: 50
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MORRISON & FOERSTER, LLP
: STREET: 2000 Pennsylvania Avenue, NW, Suite 5500
: CITY: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20006-1888
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: Windows
: SOFTWARE: FastSeq for Windows Version 2.0b
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/850,910A
: FILING DATE: 05-MAY-1997
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/477,226
: FILING DATE: 08-FEB-1990
: APPLICATION NUMBER: 07/299,880
: FILING DATE: 19-JAN-1989
: APPLICATION NUMBER: 07/206,470
: FILING DATE: 14-JUN-1988
: APPLICATION NUMBER: 07/200,383
: FILING DATE: 31-MAY-1988
: ATTORNEY/AGENT INFORMATION:
: NAME: Murashige, Kate H
: REGISTRATION NUMBER: 29,959
: REFERENCE/DOCKET NUMBER: 219002025212
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-867-1500
: TELEFAX: 202-822-0168
: TELEX:
: INFORMATION FOR SEQ ID NO: 41:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 131 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: FRAGMENT TYPE: internal
: US-08-850-910A-41

Query Match      48.5%; Score 334.5; DB 2; Length 131;
Best Local Similarity 53.0%; Pred. No. 8.9e-31;
Matches 71; Conservative 20; Mismatches 40; Indels 3; Gaps 2;

QY 1 mdpqtapsra1111f1h1a1fgrshp1gspgsasdltsq1gqgrnh1gk1se1qve 60
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 1 MGPMAAPR-VLLLFLLFLILGCRSHPLGGAGLASEL--PGIOELDLRLDRVSELOAE 57

QY 61 qtslepdgsprptgvykswrevateg1gghkmylytlraprpskmyvgsgcfcgrkndr1 120
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 58 RTDLEPLRQDGLTEANEARAAAPTVGLGPRSSIFQVLRGIRSPKTMDSGCFGRRLDRI 117

QY 121 ssssg1gckv1lrh 134
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 118 GSLSGLCGNVLRRY 131

RESULT 6
US-08-850-910A-46
: Sequence 46, Application US/08850910A

```

Page 4

APPLICANT: SEILHAMER, J. J.  
 APPLICANT: LEWICKI, J.  
 APPLICANT: SCARBOROUGH, R.M.  
 TITLE OF INVENTION: RECOMBINANT TECHNIQUES FOR  
 TITLE OF INVENTION: PRODUCTION OF BRAIN NUTRIENTIC PEPTIDE  
 NUMBER OF SEQUENCES: 50  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: MORRISON & FOERSTER, LLP  
 STREET: 2000 Pennsylvania Avenue, NW, Suite 5500  
 City: Washington  
 STATE: DC  
 COUNTRY: USA  
 ZIP: 20006-1888  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: Windows  
 SOFTWARE: FASTSEQ for Windows Version 2.0b  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/850,910A  
 FILING DATE: 05-MAY-1997  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/477,226  
 FILING DATE: 08-FEB-1990  
 APPLICATION NUMBER: 07/299,880  
 FILING DATE: 19-JAN-1989  
 APPLICATION NUMBER: 07/206,470  
 FILING DATE: 14-JUN-1988  
 APPLICATION NUMBER: 07/200,383  
 FILING DATE: 31-MAY-1988  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mularshige, Kate H  
 REGISTRATION NUMBER: 29,959  
 REFERENCE/DOCKET NUMBER: 219002025212  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-887-1500  
 TELEFAX: 202-822-0168  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 47:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 132 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 OS-08-850-910A-47

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Query Match          44.5%: Score 307; DB 2; Length 132;
Best Local Similarity 50.7%: Pred. No. 1, 2e-27.
Matches 68; Conservative 13; Mismatches 51; Indels 2; Gaps 1

QY      1 mdpqtataraalilflhlaifgrshp1gspysasdlstsg1qgrnh1gqk1selqve 60
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1 MEPCALPRALLLLFLTLSP1GGRPH1LGGRSPAS--EASASSELGRLKQAVSELQAE 58

QY      61 qts1ep1qesprpbgvwmkswrevatg1rghrkmyyltlraprskpmvqsgsgfgrkmd1 120
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      59 QLALEPLHRHSHSPAMARRGTRPGVLAIPHDSVQALRLLSPKMHKSGCGFGRLDRI 118

QY      121 sssg1qgcvt1rth 134
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      119 GSLGSLGCNVLRLKY 132

RESULT
      8
US-08-850-910A-43
: Sequence 43, Application us/08850910A
: Patent No. 5948761
: GENERAL INFORMATION:
: APPLICANT: SEITZHAMER, J.J.
: APPLICANT: LEWICKI, J.

```



ADDRESSEE: CUSHMAN, DARBY & CUSHMAN  
STREET: 1625 L STREET, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/828,450  
FILING DATE: 19920131  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: SCOTT, WATSON T  
REGISTRATION NUMBER: 26,581  
REFERENCE/DOCKET NUMBER: 9437/94133  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-861-3067  
TELEFAX: 202-822-0944  
TELEX: 6714627 CUSH  
INFORMATION FOR SEQ ID NO: 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 32 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-828-450-41

Query Match 24.5%; Score 169; DB 1; Length 32;  
Best Local Similarity 100.0%; Pred. No. 7.6e-13;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 spkmvgsqcfgrkmdrissssglgckvlrh 134  
|||||  
Db 1 SPRKVGSGCFGRKMDRISSSSGIGCKVLRH 32

RESULT 11  
US-08-297-330-2

Sequence 2, Application US/08297330  
Patent No. 5583108

GENERAL INFORMATION:

APPLICANT: Wei, Chi-Ming  
TITLE OF INVENTION: Vasoonactin Peptide and Analogs  
TITLE OF INVENTION: Thereof  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merchant & Gould  
STREET: 3100 No. 5583108west Center  
CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55402-4131

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/297,330

FILING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/025,935

FILING DATE: 03-MAR-1993

ATTORNEY/AGENT INFORMATION:  
NAME: Woessner, Warren D.

REGISTRATION NUMBER: 30,440  
REFERENCE/DOCKET NUMBER: 1016.99-US01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-332-5300  
TELEFAX: 612-332-9081  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 32 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Mature human brain natriuretic peptide  
US-08-297-330-2

Query Match 24.5%; Score 169; DB 1; Length 32;  
Best Local Similarity 100.0%; Pred. No. 7.6e-13;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 spkmvgsqcfgrkmdrissssglgckvlrh 134  
|||||  
Db 1 SPRKVGSGCFGRKMDRISSSSGIGCKVLRH 32

RESULT 12  
US-08-451-240-22

Sequence 22, Application US/08451240  
Patent No. 5665704

GENERAL INFORMATION:

APPLICANT: Lowe, David  
APPLICANT: Cunningham, Brian  
APPLICANT: Oare, David  
APPLICANT: McDowell, Robert S.  
TITLE OF INVENTION: RECEPTOR SPECIFIC ATRIAL NATRIURETIC  
TITLE OF INVENTION: PEPTIDES  
NUMBER OF SEQUENCES: 47  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/451,240

FILING DATE:

CLASSIFICATION: 530

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/362552

FILING DATE: 06-JAN-1995

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/152994

FILING DATE: 12-NOV-1993

ATTORNEY/AGENT INFORMATION:  
NAME: Kudinec, Jeffrey S.

REGISTRATION NUMBER: 36,575

REFERENCE/DOCKET NUMBER: P0844P1C1

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-8228

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 32 amino acids

TYPE: amino acid  
TOPOLOGY: linear  
US-08-451-240-22

Query Match 24.5%; Score 169; DB 1; Length 32;  
Best Local Similarity 100.0%; Pred. No. 7.6e-13;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 spkmvqsgcfcgrkmdrissssglgckvllrrh 134  
|||||  
DB 1 SPKMVQSGCFCGRKMDRISSSSGLGCKVLLRRH 32

RESULT 13  
US-08-470-846A-3

Sequence 3, Application US/08470846A  
Patent No. 5846932

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.

APPLICANT: Lowe, David G.

APPLICANT: Cunningham, Brian C.

APPLICANT: Oare, David

APPLICANT: McDowell, Robert S.

TITLE OF INVENTION: RECEPTOR SPECIFIC ATRIAL NATRIURETIC PEPTIDES

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpatlin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/470,846A

FILING DATE: 06-Jun-1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/419877

FILING DATE: 11-APR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/362552

FILING DATE: 06-JAN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/152994

FILING DATE: 12-NOV-1993

ATTORNEY/AGENT INFORMATION:

NAME: Rubinec, Jeffrey S.

REGISTRATION NUMBER: 36,575

REFERENCE/DOCKET NUMBER: P0844P2C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-8228

TELEFAX: 415/252-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 32 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

US-08-470-846A-3

Query Match 24.5%; Score 169; DB 2; Length 32;  
Best Local Similarity 100.0%; Pred. No. 7.6e-13;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 spkmvqsgcfcgrkmdrissssglgckvllrrh 134

DB 1 SPKMVQSGCFCGRKMDRISSSSGLGCKVLLRRH 32  
|||||

RESULT 14  
PCT-US94-02391-2

Sequence 2, Application PC/TUS9402391

GENERAL INFORMATION:

APPLICANT: Mayo Foundation for Medical Education and Research

APPLICANT: 200 First Street S.W. 55905 USA

APPLICANT: Rochester, Minnesota

TITLE OF INVENTION: Vasopressin Peptide and Analogs Thereof

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Schwegman, Lundberg & Woessner

STREET: 3500 IDS Center

CITY: Minneapolis

STATE: MN

COUNTRY: USA

ZIP: 55402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentlin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/02391

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/025,935

FILING DATE: 03-MAR-1993

ATTORNEY/AGENT INFORMATION:

NAME: Woessner, Warren D.

REGISTRATION NUMBER: 30,440

REFERENCE/DOCKET NUMBER: 150.99US01

TELECOMMUNICATION INFORMATION:

TELEPHONE: 612-339-3061

TELEFAX: 612-339-3061

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 32 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

PCT-US94-02391-2

Query Match 24.5%; Score 169; DB 4; Length 32;  
Best Local Similarity 100.0%; Pred. No. 7.6e-13;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 spkmvqsgcfcgrkmdrissssglgckvllrrh 134  
|||||  
DB 1 SPKMVQSGCFCGRKMDRISSSSGLGCKVLLRRH 32

RESULT 15  
PCT-US94-12591-22

Sequence 22, Application PC/TUS9412591

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.

APPLICANT: Cunningham, Brian C.

APPLICANT: Oare, David

APPLICANT: McDowell, Robert S.

APPLICANT: Burnier, John

TITLE OF INVENTION: RECEPTOR SPECIFIC ATRIAL NATRIURETIC

NUMBER OF SEQUENCES: 47

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd  
 CITY: South San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94080  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: patin (Genentech)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US94/12591  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/152994  
 FILING DATE: 12-NOV-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Winter, Daryl B.  
 REGISTRATION NUMBER: 32,637  
 REFERENCE/DOCKET NUMBER: 844P1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415/225-1249  
 TELEFAX: 415/952-9881  
 TELEX: 910/371-7168  
 INFORMATION FOR SEQ ID NO: 22:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 32 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 PCT-US94-12591-22

Query Match 24.5%; Score 169; DB 4; Length 32;  
 Best Local Similarity 100.0%; Pred. No. 7 6e-13;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 103 spkmvqsgcfcgrkmdrissssgigckvlrrh 134  
 Db 1 spkmvqsgcfcgrkmdrissssgigckvlrrh 32

Search completed: April 27, 2000, 18:34:45  
 Job time: 3059 sec







RT		Cloning of an unusual natriuretic peptide from the south American coral snake Micrurus corallinus. <sup>#</sup> ; Eur. J. Biochem. 250:144-149(1997).					
RL							
DR	EMBL; U77596;	AAC60341.1:-	-				
DR	PROSITE; PS00263;	NATRIURETIC_PEPTIDE; 1.					
DR	PFAM; PF00212;	ANP; 1.					
DR	PRINTS; PR00710;	NATPEPTIDES.					
SQ	SEQUENCE	139 AA;	14881 MW;	05421ABB CRC32;			
	Query Match	13.1%;	Score 90.5;	DB 13;	Length 139;		
	Best Local Similarity	31.9%;	Pred. No. 0.064;				
	Matches 23;	Conservative	9;	Mismatches 25;	Indels 15;	Gaps	
Qy	61 qtsleplqesprptgtwksrevatagirghrkmyltlraprspkmvgsgcfgrkmdri	120   :   :       :	:           :				
Db	50 QAVLDPWHPERPAG-----SGDDGDSR-----RLEGLAKEALGDGCFGQRIDRI	94					
Qy	121 sssslgckvrlr	132 :     :   :					
Db	95 CNVSGMGCNHVR	106					
RESULT	8						
QY92Y4							
ID	Q9Y2Y4	PRELIMINARY;	PRT;	487	AA.		
DC	Q9Y2Y4:						
DT	01-NOV-1999	(TREMBLrel. 12,	Created)				
DT	01-NOV-1999	(TREMBLrel. 12,	Last sequence update)				
DT	01-NOV-1999	(TREMBLrel. 12,	Last annotation update)				

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DE TESTIS ZINC FINGER PROTEIN.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RA TANG T.K., LAI C.-H., TANG C.-J., HUANG C.-J., LIN W.-C.;
RT "Identification and gene structure of a novel human PLZF related
RT transcription factor gene, TZFP."
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF130255; AAD27708.1; -.
SQ SEQUENCE 487 AA; 52962 MW; E3F0D6BF CRC32;

Query Match 12.4%; Score 85.5; DB 4; Length 487;
Best Local Similarity 25.2%; Pred. NO. 0.81;
Matches 33; Conservative 24; Mismatches 55; Indels 19; Gaps 5;

QY 18 hlaflgrshpplsgs---asdlsglqeqnrlhlgklselqveqtsleplqesprpt 74
DB 43 HSLVLGVQSLQRRGQWALGEGISPTFAQLNLFVYGESVELQPGF--LRPLQEAARAL 100
QY 75 qv-----wksr-----evateglgrkmvlytlraprskpkmvggscfgrkmdriss 123
DB 101 GVOSLEACHWRAGDRAKKPDGLKKHOE---BPEKPSRNPRELGDGPGKQPEQVSR 157
QY 124 sglgckvlrrh 134
DB 158 GGREQEMLHKH 168

RESULT 9
O70373 PRELIMINARY; PRT; 1677 AA.
AC O70373
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE XIN.
GN XIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CARDIAC MUSCLE;
RA WANG D.-Z., HU X., LIN J.L.-C., KITTEN G.T., SOLURSH M., LIN J.J.-C.;
RL Front. Biosci. 1:0-0(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=CARDIAC MUSCLE;
RA WANG D.-Z., LIN J.J.-C.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF051945; AAC06023.1; -.
DR MGD: MGI:1333878; Xin.
SQ SEQUENCE 1677 AA; 182085 MW; 106A30FA CRC32;

Query Match 11.8%; Score 81.5; DB 11; Length 1677;
Best Local Similarity 25.8%; Pred. NO. 8;
Matches 24; Conservative 15; Mismatches 35; Indels 19; Gaps 2;

QY 47 rnhlqgklselqveqtsleplqesprptgwkrevateg-----irg 89
DB 109 RGLPLGNLCQVATSRPPLSLRKLAPLTAQIRSRRTSRSGDVQAAQMPETKPLDALRG 168
QY 90 hrkmvlytlraprskpkmvggscf--grkmdri 120
DB 169 QEATQTTMREPATGDVQGTAKLFEPLDRL 201

RESULT 10

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O82861 PRELIMINARY; PRT; 1326 AA.
AC O82861
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE CELLULOSE SYNTHASE SUBUNIT C.
GN BCSC.
OS Acetobacter xylinum (Acetobacter pasteurianus).
OC Bacteria; Proteobacteria; alpha subdivision; Acetobacteraceae;
OC Acetobacter.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BPR2001;
RA UMEYAMA T., TONOUCHI N.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BPR2001;
RX MEDLINE: 98296257.
RA NAKAI T., MORIYA A., TONOUCHI N., TSUCHIDA T., YOSHINAGA F.,
RA HORINOCHI S., SONE Y., MORI H., SAKAI F., HAYASHI T.;
RT "Control of expression by the cellulose synthase (bcsA) promoter
RT region from Acetobacter xylinum BPR 2001."
RL Gene 213:93-100(1998).
DR EMBL: AB010645; BAA31465.1; -.
SQ SEQUENCE 1326 AA; 142103 MW; F49C1753 CRC32;

Query Match 11.4%; Score 78.5; DB 2; Length 1326;
Best Local Similarity 24.0%; Pred. NO. 12;
Matches 29; Conservative 19; Mismatches 50; Indels 23; Gaps 4;

QY 2 dpq-tapsrallllflhlaflgrshpplsggsasdlsglqeqnrlhlgklselqve 60
DB 731 DPEATSPKLALRYNGH-----GKPGKALEIDLAIVLRHPQLDARAAVQAA 779
QY 61 qts-----leplqesprptgwkrevateglgrkmvlytlraprskpkmvggs 110
DB 780 VNSNHSLATRLAMDGVQSPMDARAWLAMAVADQA-DGHGQRTIEDLRAYDLRLQYVE 838
QY 111 g 111
DB 839 G 839

RESULT 11
Q28644 PRELIMINARY; PRT; 1984 AA.
AC Q28644
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE SODIUM CHANNEL ALPHA-SUBUNIT.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Lagomorpha; Leporidae; Oryctolagus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NEW ZEALAND WHITE; TISSUE=SCIATIC NERVE;
RX MEDLINE: 96074641.
RA BELCHER S.M., ZERILLO C.A., LEVENSON R., RITCHIE J.M., HOWE J.R.;
RT "Cloning of a sodium channel alpha subunit from rabbit Schwann
RT cells."
RL Proc. Natl. Acad. Sci. U.S.A. 92:11034-11038(1995).
DR EMBL: U35238; AAA89159.1; -.
DR PFAM: PF00520; Ion_trans; 4.
DR PFAM: PF00612; IQ; 1.
DR PRINTS: PR00170; NACHANNEL.
KW Ionic channel.
SQ SEQUENCE 1984 AA; 225748 MW; EF89D962 CRC32;

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Query Match	10.9%	Score 75.5;	DB 12;	Length 780;
Best Local Similarity	27.4%;	Pred. No. 14;		
Matches	29;	Conservative 13;	Mismatches 47;	Indels 17; Gaps 3;

  

QY	12	llllflblaf--lgrshpbgpsasdsletsglgeqrnhhgkklseiqvqtslepiqe	69
Db	680	ILRLFFKAFNMWLSAKPRYPVIGKAYNNLT-----KNDLENMLDNWEISRTNLKTCKE	733
QY	70	spriptgwksrevateglgrhkmvlytlrapgpmvgsgscgr	115
Db	734	-----LRKALTEASRRARKOTIYKLGSDISLSVSEYGVFGQ	770

  

RESULT	13
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ID	Q921P7
AC	Q921P7
DC	PRELIMINARY;
PR	791 AA.
DT	01-MAY-1999 (TrEMBLrel. 10, Created)
DT	01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT	01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE	NG28.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Mammalia;
OC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=129;
RC	ROWEN L., QIN S., MADAN A., LORETZ C., HALL J., JAMES R., DORS M.,
RC	SHAFFER T., ABBASI N., RATCLIFFE A., DICKHOFF R., LASKY S., HOOD L.;
RT	"Sequence of the mouse major histocompatibility complex class II
RT	region.,"
RL	Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AF110520; AAC97966.1; -.
DR	HSSP; P42773; 1BU9.
DR	SEQUENCE 791 AA; 84186 MW; 495A3736 CRC32;
SQ	

Query Match	10.8%	Score	74.5;	DB	2;	Length	418;
Best Local Similarity	24.5%;	Pred.	NO. 8.7;				
Matches	38;	Conservative	10;	Mismatches	42;	Indels	65;
Gaps							
Qy	7	psralllllfhlaf1-----	ggrshplsgpgsaadletsqgcqrnhlgk1	54			
		: :	:	:			
Db	224	PTRRRLLAGLQLSEHAPANRGLADTRDGRHRPH-AMP-	---QRPLRRQR---	QTPL	273		
Qy	55	selsvgeqtsleplgesp----					
		: :	:	:			
Db	274	PLVOMRQDLLEPLPQPVDLAHNRPAPTRLKQNTMLLPYSHSFGSVATRPAGW--R	331				
Qy	81	evategirghrkmvlytlraprspkvmvgsgcfr	115				
		. :	:	:			
Db	332	RSPTGRRARR-----	RSPTAPRTNRRGPATGR	359			
		: :	:	:			
RESULT	15						
O18212		PRELIMINARY;	PRT;	557 AA.			
ID	O18212						
AC	O18212;						
DT	01-JAN-1998 (TEMBREL. 05, Created)						
DT	01-JAN-1998 (TEMBREL. 05, Last sequence update)						
DT	01-JAN-1999 (TEMBREL. 09, Last annotation update)						
DE	Y53C12A.3 PROTEIN.						
GN	Y53C12A.3.						
OS	Caenorhabditis elegans.						
OC	Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditiia; Rhabditida;						
OC	Rhabditiina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.						
[1]							
RN	SEQUENCE FROM N.A.						
RP	KERSHAW J., LENNARD N.;						
RA							

	Query Match	10.8%	Score	74.5;	DB	2;	Length	418;								
	Best Local Similarity	24.5%;	Pred.	NO. 8.7;	Mismatches	38;	Conservative	10;								
								Gaps								
Oy	7	pssrlllflfhlafl-----ggrshplsgpsasdlstslgcqrnhlgkkl 54                       :           Db	224	PTRRRLUAGLQLESHAPANRGLADTRDGRHPHP-AMP-----QRPLRRQR---QTPL 273                       :	Oy	55	selsvqegtsleplgesp-----rrtggvwksr 80   :         :   :   :   :   :   :	Db	274	PLVOMRQDLPLELPQPVDLAHNRPAPTRLKQNTMLLPYSHSFGSVATRPAGW--R 331   :	Oy	81	eivategirhkrmlytlraprspkmvgsgcfr 115                     :   :   :   :	Db	332	RSPTGRRARR-----RSPTAPRTNRGRPATGR 359   :
RESULT 15																
OI	R8212	PRELIMINARY; PRT; 557 AA.														
AC	OI8212;															
DT	01-JAN-1998 (T-EMBLrel. 05, Created)															
DT	01-JAN-1998 (T-EMBLrel. 05, Last sequence update)															
DT	01-JAN-1999 (T-EMBLrel. 09, Last annotation update)															
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GN	Y53C12A.3.															
OS	Caenorhabditis elegans.															
OC	Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditiia; Rhabditida;															
OC	Rhabditiina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.															
[1]																
RN	SEQUENCE FROM N.A.															
RP	KERSHAW J., LENNARD N.;															
RA																



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: April 27, 2000, 20:11:09 ; Search time 386.23 Seconds  
(without alignments)  
-3160.361 Million cell updates/sec

Title: SEQ1  
Perfect score: 402  
Sequence: 1 atggtcccccagacagcacc.....gcaaaagtgtgagggcgcat 402  
Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0  
Searched: 821193 seqs, -1518192014 residues  
Total number of hits satisfying chosen parameters: 1642386  
Minimum DB seq length: 0  
Maximum DB seq length: 1000000  
Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb\_ba1.\*
- 2: gb\_ba2.\*
- 3: gb\_om.\*
- 4: gb\_ov.\*
- 5: gb\_pat.\*
- 6: gb\_ph.\*
- 7: gb\_pl1.\*
- 8: gb\_pl2.\*
- 9: gb\_pr1.\*
- 10: gb\_pr2.\*
- 11: gb\_pr3.\*
- 12: gb\_ro.\*
- 13: gb\_sts.\*
- 14: gb\_sy.\*
- 15: gb\_un.\*
- 16: gb\_vi.\*
- 17: em\_fun.\*
- 18: em\_hum1.\*
- 19: em\_hum2.\*
- 20: em\_in.\*
- 21: em\_om.\*
- 22: em\_or.\*
- 23: em\_ov.\*
- 24: em\_pat.\*
- 25: em\_ph.\*
- 26: em\_pl.\*
- 27: em\_ro.\*
- 28: em\_sts.\*
- 29: em\_sy.\*
- 30: em\_un.\*
- 31: em\_v1.\*
- 32: gb\_htg1.\*
- 33: gb\_htg2.\*
- 34: gb\_in1.\*
- 35: gb\_in2.\*
- 36: em\_ba1.\*
- 37: em\_ba2.\*
- 38: em\_hum3.\*
- 39: em\_hum4.\*
- 40: gb\_pr4.\*
- 41: gb\_htg3.\*
- 42: gb\_htg4.\*
- 43: gb\_htg5.\*
- 44: gb\_htg6.\*

- 45: gb\_htg7.\*
- 46: em\_htg1.\*
- 47: em\_htg2.\*
- 48: em\_htg3.\*
- 49: em\_hum5.\*
- 50: gb\_pl3.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	402	100.0	692	5	E02602
2	402	100.0	692	9	HUMNATPEP
3	320.8	79.8	888	5	E04396
4	320.8	79.8	888	5	E04438
5	260.4	64.8	1922	9	HUMBNPA
6	260.4	64.8	107603	11	HS934G17
7	180.6	44.9	669	5	E02565
8	180.6	44.9	670	3	PIGBNP
9	165	41.0	732	5	E04397
10	165	41.0	732	5	E04439
11	139	34.6	1479	3	PIGBNPA
12	132.4	32.9	331	13	G09534
13	120.4	30.0	2125	3	AF037466
14	116.4	29.0	1803	3	DOGNBPA
15	96	23.9	96	5	E05300
16	81.2	20.2	603	5	E08239
17	81.2	20.2	603	12	HAMBNPB
18	60.2	15.0	628	5	E02718
19	60.2	15.0	628	12	RATBNP
20	53.8	13.4	1301	12	RATISOANP
21	53.8	13.4	2575	12	RATISO
22	52.4	13.0	755	4	GGNATRIUP
23	52.4	13.0	755	5	E02222
24	52	12.9	96	5	E05301
25	51	12.7	828	5	E07271
26	51	12.7	831	5	E07269
27	47.8	11.9	1432	12	S58667
28	47.8	11.9	1449	12	D82049
29	47.8	11.9	1465	5	E07272
30	47.8	11.9	1468	5	E07270
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32	42	10.4	2931	40	AF193421
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35	40.8	10.1	177998	40	AC006977
36	39.8	9.9	1926	5	AR001353
37	39.8	9.9	1926	5	AR002249
38	39.8	9.9	1926	5	AR065918
39	39.8	9.9	1926	5	I56650
40	39.8	9.9	1926	5	I58413
41	39.8	9.9	1926	5	I79529
42	39.8	9.9	1926	5	I96044
43	39.6	9.9	673	3	RABANFA
44	39.2	9.8	166723	33	HS310013
45	38.6	9.6	1722	4	D85843

ALIGNMENTS

RESULT 1  
LOCUS E02602  
DEFINITION DNA encoding human brain natriuretic peptide(human BNP).  
ACCESSION E02602  
VERSION E02602.1  
KEYWORDS JP 1990231082-A/1.  
PAT 29-SEP-1997





ACCESSION	STs and the genomic marker DIS2740, complete sequence.
VERSION	AL021155
KEYWORDS	AL021155.1 GI:3171888 HTG; ANP; ANP; Atrial Natriuretic Factor; Atrial Natriuretic peptide; BNP; Brain Natriuretic Protein; chloride channel; CLC-6; CLCN6; DIS2740; KIA0046; Myotubularin-related protein; NPPA; SBFL1; human.
SOURCE	
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 107603) Errington,H. Direct Submission Submitted (12-MAY-1998) Chromosome 1 Project Group ( <a href="http://www.sanger.ac.uk/HGP/Chr1/">http://www.sanger.ac.uk/HGP/Chr1/</a> ) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquires: <a href="mailto:humquery@sanger.ac.uk">humquery@sanger.ac.uk</a> Clone requests: <a href="mailto:clonerequests@sanger.ac.uk">clonerequests@sanger.ac.uk</a> On Jun 2, 1998 this sequence version replaced gi:2769553. IMPORTANT: This sequence is the entire insert of clone 934G17. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variations annotated may not be found in the sequence submission corresponding to the overlapping clone as we submit sequences with only a small overlap as described above. This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre chromosome 1 mapping group. Further information can be found at <a href="http://www.sanger.ac.uk/HGP/Chr1/">http://www.sanger.ac.uk/HGP/Chr1/</a> This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. The true left end of clone 934G17 is at 1 in this sequence. The true right end of clone 934G17 is at 107603. 934G17 is from the library RPCR15 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see <a href="http://pacpac.med.buffalo.edu/">http://pacpac.med.buffalo.edu/</a> .
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	

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FEATURES
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T97200 F07103 AA806700 T97201 AA488792 AA046481 AA3366116
HA7501 RA231539 F03382 H83350 AA025387 AT72135 N20380
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RESULT 7

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QY 181 cagacatccctggagccctccagagagccccctccacaggtgtctggaagtcctccg 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 265 CGGACGACCTGGAGCCCTCCGCGAGACCGTGGCTCACAGAGCCTGGGAGGCGAGG 324

QY 241 gaggtagcacccagggatccctgggacccgcaaaatggtctctacacccctgcgggca 300
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Db 325 GAAGCAGCCCCCAGGGGTCTTGGGCCCGCGAGTAGCATCTCCAAGTCTCTCCGGGGA 384

QY 301 ccacgaagcccaagatggtgcaaggctgctgcttgggaggaagatggaccgcatc 360
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Db 385 ATACGAGCCCCCAGAGTGCCTGACTGTGGCTGTCTTGGCGGAGGTGGACCGGATC 444

QY 361 agctctccagtggctgggctgcaaaagtgtgagcgcca 401
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Db 445 GGCTCCTCAGCGCCTGGGCTGCAATGTGCTCAGGAGGTA 485

RESULT 9
E04397 732 bp RNA PAT 29-SEP-1997
LOCUS DNA sequence encoding human brain natriuretic peptide.
DEFINITION E04397
ACCESSION E04397
VERSION E04397.1 GI:2172598
KEYWORDS JP 1993056794-A/2.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 732)
Mor1,T., Maekawa,K., Izumi,A. and Sudo,T.
PRODUCTION OF PHYSIOLOGICALLY ACTIVE PEPTIDE
Patent: JP 1993056794-A 2 09-MAR-1993;
DAI ICHI PURE CHEM CO LTD, DAI ICHI SEIYAKU CO LTD
COMMENT OS Homo sapiens (human)
PN JP 1993056794-A/2
PD 09-MAR-1993
PF 03-SEP-1991 JP 1991222783
PI MORI TOKUO, MAEKAWA KEIJI, IZUMI ATSUSHI, SUDO TETSUJI PC
C12P21/02,C12N15/62,C12N15/70/A61K37/02,A61K37/02,A61K37/02, PC
C07K7/10.
PC (C12P21/02,C12R1:19),C07K99:00;
CC strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
CC Location/Qualifiers
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    /db_xref="taxon:9606"
BASE COUNT 204 a 180 c 174 g 174 t
ORIGIN

Query Match 41.0%; Score 165; DB 5; Length 732;
Best Local Similarity 85.9%; Pred. No. 7.6e-32;
Matches 183; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 190 ctggagccctccagagagccccctccacaggtgtctggaagtcctccggaggtagcc 249
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Db 421 CAGGTGCACCTGGCAGCGGACTGCCCTCCATGATAGATTCCAGATCCGGGAGGTAGCC 480

QY 250 accgagggcatccgtggcaccgcaaaatggtctctacacccctgggacaccagcgaac 309
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 481 ACCGAGGGCATCCGTGGGACCGCAAAATGGTCTCTACACCTGCGGGGACCCAGAGAC 540

QY 310 cccaagatggtgcaaggctgctgcttgggaggaagatggaccggatcagctctccc 369
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Db 541 CCCAAGATGGTGCAGGGGTCTGGCTGTGGAGGAAGATGGACCGGATCAGCTCCTCC 600

QY 370 agtgccctggctgcaaaagtgtctgagcgccat 402
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Db 601 AGTGCCCTGGGCTGCAAAAGTGTCTGAGGCGGCAT 633

RESULT 11
E04439 732 bp RNA PAT 29-SEP-1997
LOCUS DNA encoding recombinant hBNP(human Brain Natriuretic Peptide).
DEFINITION E04439
ACCESSION E04439
VERSION E04439.1 GI:2172640
KEYWORDS JP 1993068581-A/2.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 732)
Mor1,T., Maekawa,K., Izumi,A. and Sudo,T.
PRODUCTION OF PHYSIOLOGICALLY ACTIVE PEPTIDE
Patent: JP 1993068581-A 2 23-MAR-1993;
DAI ICHI PURE CHEM CO LTD, DAI ICHI SEIYAKU CO LTD
COMMENT OS Homo sapiens (human)
PN JP 1993068581-A/2
PD 23-MAR-1993
PF 10-SEP-1991 JP 1991230597
PI MORI TOKUO, MAEKAWA KEIJI, IZUMI ATSUSHI, SUDO TETSUJI PC
C12P21/02,C12N15/62/A61K37/02,A61K37/02,A61K37/02,C07K7/10, PC
(C12P21/02,
PC C12R1:19),C07K99:00;
CC strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
CC *source: clone-pKKriNb;
CC Location/Qualifiers
FEATURES
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    /db_xref="taxon:9606"
BASE COUNT 204 a 180 c 174 g 174 t
ORIGIN

Query Match 41.0%; Score 165; DB 5; Length 732;
Best Local Similarity 85.9%; Pred. No. 7.6e-32;
Matches 183; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 190 ctggagccctccagagagccccctccacaggtgtctggaagtcctccggaggtagcc 249
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Db 421 CAGGTGCACCTGGCAGCGGACTGCCCTCCATGATAGATTTCAGATCCGGGAGGTAGCC 480

QY 250 accgagggcatccgtggcaccgcaaaatggtctctacacccctgggacaccagcgaac 309
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Db 481 ACCGAGGGCATCCGTGGGACCGCAAAATGGTCTCTACACCTGCGGGGACCCAGAGAC 540

QY 310 cccaagatggtgcaaggctgctgcttgggaggaagatggaccggatcagctctccc 369
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 541 CCCAAGATGGTGCAGGGGTCTGGCTGTGGAGGAAGATGGACCGGATCAGCTCCTCC 600

QY 370 agtgccctggctgcaaaagtgtctgagcgccat 402
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Db 601 AGTGCCCTGGGCTGCAAAAGTGTCTGAGGCGGCAT 633

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Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
1 (bases 1 to 1479)  
Porter, J.G., Arsten, A.E., Palisi, T., Scarborough, R.M.,  
Lewicki, J.A., and Sellhammer, J.J.  
Cloning of a cDNA encoding porcine brain natriuretic peptide  
J. Biol. Chem. 264, 6689-6692 (1989)  
89214071  
Draft entry and computer-readable sequence [1] kindly submitted by  
J.J. Sellhammer, 09-FEB-1989.  
Location/Qualifiers  
1..1479  
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/tissue\_type="atrium"  
<1..218  
/gene="BNP"  
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/protein\_id="AAA31007.1"  
/db\_xref="GI:164393"  
/translation="MGPRALPRVLLLFHLLLCGRSHPLGAGLASELPQIGELL  
DRLDVSEIQAEITDLELRQGLTEAWEREAAPTGLVGRSSIFQVLRIRSPK  
TMRDSCGFGRLDRIGLSGLGCVLRY"  
217..462  
/gene="BNP"  
/number=1  
463..718  
/gene="BNP"  
/number=2  
640..717  
/gene="BNP"  
/product="brain natriuretic peptide"  
719..1272  
/gene="BNP"  
/number=2  
303 a 448 c 404 g 324 t  
BASE COUNT 303 a 448 c 404 g 324 t  
ORIGIN  
Query Match 34.68; Score 139; DB 3; Length 1479;  
Best Local Similarity 71.08; Pred. No. 2.5e-25;  
Matches 184; Conservative 0; Mismatches 75; Indels 0; Gaps 0;  
QY 130 caggagcagcgaacatttcagggaacactgtcggagctgcaggtaggagcagacatcc 189  
DB 460 caggagctgtcggccgctcggagacagggtctccgagctgcaggcggcggcggcggc 519  
QY 190 ctggagccctccaggagagcccgctccacaggtgtctggaagtcgccgggaggtagcc 249  
DB 520 CTGGAGCCCTCCGGCAGGACCGTGGCTCAGAGAGCTGGAGGCGAGGAGGAGCAGCC 579  
QY 250 accagggcctccgtgggacccgcaaaatggtctctctacacccctgcggggacccagcga 309  
DB 580 CCCACGGGGGTCTTGGGCCCGCAGTAGTACATCTTCCAAAGTCCCTCCGGGAATACGCAGC 639  
QY 310 cccaagatggtgcaaggtctggtctgttggaggaagatggaccgagatcagctctcc 369  
DB 640 CCCAAGACATGCGTACTCTGGTCTGCTTTGGCGGAGGCTGGACCGATCGGCTCCCTC 699  
QY 370 agtggcctgggctgcaag 388  
DB 700 AGCGGCTGGGCTGCAATG 718  
RESULT. 12  
G09534

LOCUS G09534 331 bp DNA STS 15-AUG-1995  
human STS CHLC.GCT3H01.P11079 clone GCT3H01.  
G09534  
G09534.1 GI:941383  
STS sequence; primer; sequence tagged site.  
human vector-pJCP1 host-E.coli dut+ung+ (DH10B) Marker Selected  
genomic DNA prepared from xy individual of French nationality.  
ORGANISM Homo sapiens  
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata;  
Cetartiodactyla; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;  
Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 331)  
AUTHORS Murray J., Sheffield, V., Weber, J.L., Duyk, G. and Buetow, K.H.  
TITLE Cooperative Human Linkage Center  
JOURNAL Unpublished (1995)  
COMMENT Synonyms: GCT3H01, CHLC.GCT3H01.T11078  
Contact: Dr. Jeffrey C. Murray  
UofI  
The University of Iowa  
Department of Pediatrics, Iowa City, IA 52242, USA  
Tel: (319) 356-3508  
Fax: (319) 356-3347  
Email: jeff-murray@uiowa.edu  
Primer A: AGGAGCCAGGAGGAGGAGC  
Primer B: ATCCATGCTCTGGAGGAC  
STS size: 124  
PCR Profile:  
denature: 30 seconds at 94 degrees C  
annealing: 75 seconds at 55 degrees C  
extension: 15 seconds at 72 degrees C  
PCR cycles: 27  
extension: 6 minutes at 72 degrees C  
Protocol:  
Template: 30ng genomic DNA  
primer: each 1.5 pmole  
dNTPs: each 200 uM  
Tag Polymerase: 0.3 units  
Total Vol: 10 ul  
Buffer:  
MgCl2: 1.5mM  
KCl: 50mM  
Tris: 10mM  
pH: 8.3.  
FEATURES  
source Location/Qualifiers  
STS /organism="Homo sapiens"  
primer\_bind 12..135  
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BASE COUNT 68 a 104 c 106 g 50 t 3 others  
ORIGIN  
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Best Local Similarity 98.5%; Pred. No. 1.3e-23;  
Matches 133; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 atggatccccagacagcaccttcccgggcgctcctgctcctctcttcttgcattctggct 60  
DB 130 ATGGATCCCCAGACAGACACCTTCCGGGGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 189  
QY 61 ttctctgggaggttggttccacacccgctgggagcccggttcagctcggacttggaaacg 120  
DB 190 TTCCTGGAGGTCGTCTCCACCGCTGGGAGCCCGGTCAGCCTCGGACTTGGAAACG 249  
QY 121 tccgggttacaggag 135  
DB 250 TCCGGGTTACAGGTG 264

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RESULT 13
AF037466
LOCUS
DEFINITION
Ovis aries brain natriuretic peptide (BNP) gene, complete cds.
ACCESSION
AF037466
VERSION
AF037466.1 GI:2708651
KEYWORDS
sheep.
SOURCE
Ovis aries
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Caprinae; Ovis.
REFERENCE
1 (bases 1 to 2125)
Aitken, G.D., Raizis, A.M., George, P.M., Espiner, E.A. and
Cameron, V.A.
TITLE
The Characterization of Ovine Genes for Atrial, Brain and C-Type
Natriuretic Peptides
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 2125)
Aitken, G.D., Raizis, A.M., George, P.M., Espiner, E.A. and
Cameron, V.A.
AUTHORS
Direct Submission
TITLE
Submitted (08-DEC-1997) Medicine, University of Otago, Riccarton
JOURNAL
Ave, Christchurch, Canterbury, New Zealand
FEATURES
Location/Qualifiers
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/organism="Ovis aries"
/db_xref="taxon:9940"
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/product="brain natriuretic peptide"
<870..>2070
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/codon_start=1
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/db_xref="GI:2708652"
/translation="MDPKALSRLLLLFLHLSLGLGRSHPLGPGSASELPGLQEL
LRLRDRVSELQAEOLRVEPLQGGGLEETWDSRAAPAGFLGPHHSLQLALRGFKM
RDSGCFGRRLDRIGLSLGLGNCVLRKY"
-BASE COUNT 431 a 654 c 648 g 392 t
ORIGIN

Query Match 30.0%; Score 120.4; DB 3; Length 2125;
Best Local Similarity 69.5%; Pred. No. 1.2e-20;
Matches 182; Conservative 0; Mismatches 71; Indels 9; Gaps 1;

QY 127 ttacaggagcagcgcaaccatttgcaggagcgaactgtcggagctcaggtgagcagaca 186
DB 1268 TTGCAGGAGCTGTGTGACCGCTCTACGACAGACAGGGTCTCGAGCTGCGAGCGAGCAGCTG 1327
QY 187 tccttgagccctccagagagcccccctccacaggtgtctggaagtcccgaggagta 246
DB 1328 CGCGTGGAGCCCTCCAGCAGAGGCGCCCTGGAGAAACCTGGACTCCCGCGGGCA 1387
QY 247 gccaccagggatccgtgggaccccaaatggtctctacacccctggggcaccaca 306
DB 1388 GCCCCGCGGGGTCTCTGGGCCCCACACAGCCTCTCCAGGCCCTGGGG----- 1440
QY 307 agcccaagatggtgcaagggtctgtgcttttggaggagaagtggaccggatcagctcc 366
DB 1440 -GCCCAAGATGATGCGCAGCTGGGCTCTTTGGACGAGGCTGGACCGGATCGGCTCC 1498
QY 367 tccagtggcctgggtgcaag 388
DB 1499 CTCAGTGGCTGGGCTGCAACG 1520

RESULT 14
DOGBNPA
LOCUS
DEFINITION
Dog brain natriuretic protein (BNP) gene, complete cds.
ACCESSION
M31777
VERSION
M31777.1 GI:163912
KEYWORDS
Dog DNA, clone D1.
SOURCE
Canis sp.
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
1 (bases 1 to 1803)
Seilhamer, J.J., Arfsten, A.E., Miller, J.A., Lundquist, P.,
Scarborough, R.M., Lewicki, J.A. and Porter, J.G.
TITLE
Human and canine gene homologs of porcine brain natriuretic peptide
JOURNAL
Biochem. Biophys. Res. Commun. 165, 650-658 (1989)
MEDLINE
90088474
FEATURES
Location/Qualifiers
1..1803
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/db_xref="taxon:9616"
<365..517
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join(365..517,740..992,1555..1571)
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SGLNVAQELLRLKDAVSELQAEQLAEPLHRSAPRAPAGGTGPGVLAHPHDSVLQ
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-intron 518..739
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exon 740..992
/number=2
intron 993..1554
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exon 1555..>1571
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/number=3
BASE COUNT 358 a 552 c 526 g 367 t
ORIGIN

Query Match 29.0%; Score 116.4; DB 3; Length 1803;
Best Local Similarity 67.9%; Pred. NO. 1.2e-19;
Matches 178; Conservative 0; Mismatches 81; Indels 3; Gaps 1;

QY 127 ttacaggagcagcgcaaccatttgcaggagcgaactgtcggagctcaggtgagcagaca 186
DB 734 TTGCAGGAGCTGCTGGGCGCTGTGAAGACCGAGTTCAGAGCTCGAGCGAGCAGTTG 793
QY 187 tccttgagccctccagagagcccccgtccacaggtgtctggaagtcccgaggagta 246
DB 794 GCCTTGGAAACCTCTGACCGGAGCCAGAGCCCGGAGAGCCCGGAGGCC---GGAGA 850
QY 247 gccaccagggatccgtgggaccccaaatggtctctacacccctggggcaccaca 306
DB 851 AGCCCCCGTGGGTCTTGTGACCCCATGACAGTGTCTCCAGGCCCTGAGAAGACTACGC 910
QY 307 agcccaagatggtgcaagggtctgtgcttttggaggagaagtggaccggatcagctcc 366
DB 911 AGCCCCAAGATGATGCAAGTCAAGGTGCTTTGGCCGAGGCTGGACCGGATCGGCTCC 970
QY 367 tccagtggcctgggtgcaag 388
DB 971 CTCAGTGGCTGGGCTGCAATG 992

RESULT 15
E05300
LOCUS
DEFINITION
DNA encoding human natriuretic peptide.
ACCESSION
E05300
VERSION
E05300.1 GI:2173490

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KEYWORDS JP 1993207891-A/1.  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;  
Primates; Catarrhini; Hominoidea; Homo.  
REFERENCE 1 (bases 1 to 96)  
AUTHORS Yoshida, N., Shin, M., Teraoka, H., Tamaki, M., Inoue, T. and  
Watanabe, K.  
TITLE PRODUCTION OF BRAIN NATRIURETIC PEPTIDE  
JOURNAL Patent: JP 1993207891-A 1 20-AUG-1993;  
SHIONOGI & CO LTD  
COMMENT OS Homo sapiens (human)  
PN JP 1993207891-A/1  
PD 20-AUG-1993  
PF 08-WAR-1991 JP 1991043641  
PI YOSHIDA NOBUO, SHIN MASARU, TERAOKA HIROSHI, TAMAKI MIKIO, PI  
INOUE TAKESHI,  
PI WATANABE KUNIO  
PC C12P21/06.C07K13/00.C12N1/21.C12N15/16.C12N15/62.C12N15/70, PC  
C12P21/02//  
PC A61K37/02.A61K37/24.(C12N1/21.C12R1:19).(C12P21/02.C12R1:19);  
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CC topology: Linear;  
CC Feature is identified by similarity;  
FH Key Location/Qualifiers  
FT mat\_peptide 1..96  
FT Location/Qualifiers  
source 1..96  
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/db\_xref="taxon:9606"  
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ORIGIN

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Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 307 agccccaaagatggtgcaagggtctgtggtctttggagggaagatggaccggatcagctcc 366  
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Db 1 AGCCCCAAGATGTTGCAAGGGTCTGGCTTTGGAGGAGATGGACCGGATCAGCTCC 60  
|||||

Qy 367 tccagtggcctgggtgcaagtgctgagcgccat 402  
|||||  
Db 61 TCCAGTGGCTGGGCTGCAAGTGTCTGAGCGGCAT 96  
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Search completed: April 27, 2000, 22:31:04  
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